

STIC Search Report Biotech-Chem Library

STIC Database Irracking Number 1985

TO: Patricia Duffy

Location: REM-3B05/3C18

Art Unit: 1645

Thursday, July 28, 2005

Case Serial Number: 09/900766

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist REM-1A65 571-272-2527



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Duffy, Patricia

Sent:

Friday, July 22, 2005 6:51 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search 09/900,766

Importance:

High

In RE: 09/900,766

Please search SEQ ID NO:7 in commercial and interference databases.

Please print out top 100 hits in each category.

Thanks mucho.

Patricia A. Duffy, Ph.D. Art Unit 1645 Remsen 3B05; Mailbox 3C18 571-272-0855

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Searcher:
Searcher Phone: 2Date Searcher Picked up:
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Type of Search

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Interference:___ SPDI:___
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Title: Perfect score: Sequence:

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Scoring table:

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HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGCYTLHDNNRLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Lautra A.
REGISTRATION NUMBER: 30,742
REFERRICE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT_APPLICATION DATA:
RPLICATION NUMBER: US/10/267,682
RPLING DATE: 08-Oct-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown>
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMISSION
                                                                                                                                                                                                                                                                                                                             Sequence 112, Application US/10267682
Publication No. US20040033235A1
GENERAL INPORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (212) 790-909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 257 amino acids
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                        RESULT 3
US-10-267-682-112
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                                                 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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         SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                               HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                             RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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100.0%; Score 1238; DB 14; Length 233;

Best Local Similarity 100.0%; Pred. No. 6.7e-105;

Matches 233; Conservative 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abrahmsen and Goran Forsberg TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION;
APPLICANT: Per Antonsson, Per Bjork, Mikael Do
; Johan Hansson, Terje Kalland, Lars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-0ct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: Auguse 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
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25 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 84
                                                                                                                 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                         ; Sequence 188, Application US/10428817A; Publication No. US20040214783A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/0990766
Publication No. US20030039655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188
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                 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                         85 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                           EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                     145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TRANSMISSION
TRANSMISSION
TRANSMISSION
TRANSMISSION
TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1238; DB 15; Length 257; Best Local Similarity 100.0%; Pred. No. 7.6e-105; Matches 233; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
COUNTRY: USB
COUNTRY: USB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PR-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
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GENERAL INCORPORTION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE: 3847-189108
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT APPLICATION NUMBER: US 60/378,988
FRIOR PAPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-06-08
PRIOR PELING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR PLING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PLING DATE: 2002-09-01
PRIOR PLING DATE: 2002-10-01
PRIOR PLING DATE: 2002-10-02
PRIOR PLING DATE: 2002-10-02
PRIOR PLING DATE: 2002-10-02
PRIOR PLING DATE: 2003-10-03
PRIOR PLING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 188
LENGTH: 257

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Score 1238; DB 16;
Best Local Similarity 100.0%; Pred. No. 7.6e-105;
Matches 233; Conservative 0; Mismatches 0;
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Sequence 12, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                       145 EEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
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                                                                                  RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 224
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100.0%; Pred. No. 2.7e-100;
tive 0; Mismatches 0;
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CURRENT PEDICATION NUMBER: US/10/428,817A

CURRENT FILING DATE: 2003-05-05

PRIOR PEDICATION NUMBER: US 60/378,988

PRIOR FILING DATE: 2002-05-08

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US 60/406,597

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR APPLICATION NUMBER: US 60/415,310

PRIOR PILING DATE: 2002-10-01

PRIOR PRILING DATE: 2002-10-01

PRIOR PRILING DATE: 2002-10-02

PRIOR PELING DATE: 2002-10-02

PRIOR PELING DATE: 2002-10-02

PRIOR PELING DATE: 2002-10-02

PRIOR PELING DATE: 2002-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Staphylococcus aureus
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Best Local Similarity 100.
Matches 224; Conservative
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Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REPERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT PILING DATE: 2002-01-14
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                     APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: ANALSE, BOORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: PO2188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT APPLICATION NUMBER: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEISION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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Pred. No. 2.4e-102;
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PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-16
                                                                                                                                                                                                                                                                                                                                                                                                                               97.7%;
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 100.
Matches 224; Conservative
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Best Local Similarity 97.9°
Matches 228; Conservative
        APPLICANT: FORSBERG, GORAN
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LENGTH: 248
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LENGTH: 233
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                       Publication No. US20030039655A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: FORSBERG
APPLICANT: ANTONSSON, FUR
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
TITLE OF INVENTION: NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
TITLE OF INVENTION: ANOVEL ENGINEERE SUPPRANTIGEN FOR HUMAN THERAPY
TITLE OF INVENTION: ANOVEL ENGINEERE SOO, 766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENTH: 233
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APPLICANT: ERLANDSSON, EVA
APPLICANT: BRLANDSSON, PER
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REPERENCE: PO2188USO;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001.07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
LENGTH: 672
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89.4%; Score 1107; DB 10;
Best Local Similarity 89.7%; Pred. No. 6.4e-93;
Matches 209; Conservative 9; Mismatches 15;
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COTHER INFORMATION: Conjugate protein US-09-900-766-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION: (1):.(233)
COTHER INFORMATION: Chimeric Protein US-09-900-766-2
  Sequence 2, Application US/09900766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/09900766; Publication No. US20030039655A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
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US-09-900-766-1
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Publication No. US20050112141A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: FILE REFERENCE 650884
CURRENT PALLING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/650,884
PRIOR APPLICATION NUMBER: 09/650,884
PRIOR APPLICATION NUMBER: 09/650,884
PRIOR SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SQTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                       Query Match 96.0%; Score 1188; DB 16; Length 248; Best Local Similarity 100.0%; Pred. No. 2.7e-100; Matches 224; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.0%; Score 1188; DB 17; Length 248; 100.0%; Pred. No. 2.7e-100; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGLIVFHSSEGSTVSYDLFDAQQQYPDTLLRIYRDNKTINSENL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGLIVFHSSEGSTVSYDLFDAQQQYPDTLLRIYRDNKTINSENL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 224
                                                                                                                                            TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Staphylococcus aureus
US-10-937-758A-16
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 224; Conservative
                                                                                                                                                                                                     US-10-428-817A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-937-758A-16
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US-09-900-766-2
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Length 233;

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Gaps

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Indels

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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
Matthews, Thomas J.
Matthews, Thomas J.
Mild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TILLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 233;
                                                                                                                                                                                                                                                                                                                                         \
                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
82.6%; Score 1023; DB 14;
Best Local Similarity 82.0%; Pred. No. 3.1e-85;
Matches 191; Conservative 17; Mismatches 25;
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Krieger, Paul B.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMISSION
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 233 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                    COUNTRY: USA
ZIP: 77027-9095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-267-682-113
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                                                                                                                                                                       EBKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
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                                                                                   61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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9
                      1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
SEKSEEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FORSEERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BAUCNA
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: PO2188USO; 10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT APPLICATION NUMBER: US/09/900, 766
SOFTWARE: PATELING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATELIN VERSION 3.0
SEQ ID NO 4
LENGTH: 233
                                                                                                                                                                                                                                                        RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.6%; Score 1023; DB 10;
82.0%; Pred. No. 3.1e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND THEIR USE
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Publication No. US20030092894A1
                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/09900766; Publication No. US20030039655A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus sp
US-09-900-766-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.09
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-10-283-838-7
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82.6%; Score 1023; DB 15;
82.0%; Pred. No. 3.5e-85;
tive 17; Mismatches 25;
                   of the Americas
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SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10354948 Publication No. US20030202962A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS:
                      Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 82.09
Matches 191; Conservative
                   STREET: 1155 A.
CITY: New York
                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-354-948-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 EEKKVPINLWLDGKQNTVPLETVKTNKRNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 113, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bologomest, Dani P.
Matthews, Thomas J.
Mild, Carl T.
Mild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TRANSMASSION
TRANSMASSION
TRANSMASSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTLFKGFFTD 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.6%; Score 1023; DB 15; Length 257; 82.0%; Pred. No. 3.5e-85; tive 17; Mismatches 25; Indels 0
                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM FOC COMPATIBLE
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 113:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown>
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 82.0%
Matches 191; Conservative
                 CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
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APPLICANT: Dow, Steve W.

Elmslie, Robyn E.

PUTLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13

CORRESONDENCES: ADDRESSE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 257;
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS Compatible
COMPUTER: IS PECCOMPATIBLE
COMPUTER: IS PECCOMPATIBLE
COMPUTER: IS PECCOMPATIBLE
COMPUTER: IS PECCOMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NAMER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION NUMBER: US/08/484,223A
PRILATING DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: O7-JUN-1995
ATTORNY/AGENT INFORMATION:
NAME: CCTUZZI, LAUYE A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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SEKSEEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 166
SOFWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 257
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US-09-751-708A-8
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE REPERENCE: 970759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLTE 121
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                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 1013; DB 9;
81.5%; Pred. No. 2.9e-84;
iive 17; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1019; DB 15;
Pred. No. 7.1e-85;
                                                                                                                                                                                                                             NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4
                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 233 amino acids TYPE: amino acid
                                                                                                                                                                                           FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Staphylococcus aureus US-09-870-759-8
                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.3%;
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Best Local Similarity 81.5
Matches 190; Conservative
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Best Local Similarity 81.9
Matches 190; Conservative
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US-09-870-759-8
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Sequence 4, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPRENCE: 38137-489118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR APPLICATION NUMBER: US 60/378,366
PRIOR FILING DATE: 2002-06-08
PRIOR FILING DATE: 2002-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TERMAN, DAVIG S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751, 708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
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                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                 145 EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 204
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25 SEKSBEINEKDLRKKSBLQGAALGNLKQIYYYNBKAKTENKESHDQFLQHTILFKGFFTN
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                                                                                                                                                                                                                                                                                                                                                       Length 257;
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CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                 181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2
                                                                       205 RGLIVFHISTEPSVNYDLFGAQGONSNTLLRIYRDNKTINSENWHIDIYLYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.8%; Score 1000; DB 14; Length 257; Best Local Similarity 80.7%; Pred. No. 4.4e-83; Matches 188; Conservative 17; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                   /33

APPLICANT: Ulrich, Robert G.
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR APPLICATION NUMBER: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 2
LENGTH: 257
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ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10767687

Publication No. US20050064526A1

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,

Mark A. Olson

Sina Bavari

TITLE OF INVENTION: Bacterial Su,
                                                                                                                                                                                                           Sequence 2, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
                                                                                                                                                                      RESULT 22
US-10-002-784A-2
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Publication No. US20050112141A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/937,758A
CURRENT FILING DATE: 2004-09-08
PRIOR FILING DATE: 2004-09-08
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOCTUMER: Patentin version 3.1
LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SEKSEEINEKDLRKKKSELQGAALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTN 84
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Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.8%; Score 1013; DB 16
Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26
                 PRIOR FILING DATE: 2002-08-28
PRIOR PELLING DATE: 2002-08-28
PRIOR PILING DATE: 2002-08-28
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR PILING DATE: 2002-10-03
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin version 3.2
  APPLICATION NUMBER: US 60/406,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus aureus
US-10-937-758A-8
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                      US-10-428-817A-4
                                                                                                                                                                                                                                                                                                                 LENGTH: 257
                                                                                                                                                                                                                                                                                        SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic US-10-002-784A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.8%; Score 1000; DB 17; Length 257; Best Local Similarity 80.7%; Pred. No. 4.4e-83; Matches 188; Conservative 17; Mismatches 28; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

80.5%; Score 996; DB 14;
Best Local Similarity 80.6%; Pred. No. 9.1e-83;
Matches 187; Conservative 17; Mismatches 28;
                                                                         CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
RECISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKNOWN>
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 619-2065
TELEFAX: (301) 619-7144
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-767-687-2
      SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-002-784A-4
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LENGTH: 233
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
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                                                                                          EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
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2 EKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTDH
                                                                   62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                    182 GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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80.6%; Pred. No. 9.1e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/767,687

FILING DATE: 29-3an-2004

CLASSIFICATION: CURROWN:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/882,431B
FILING DATE: Jue 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKnown>
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SECUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.61
Matches 187, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301)
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TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: John Moran
STREET: US ATHY WRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : John Moran
US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
                                                                                                                                                                                         STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-501
ZUP: 21702-501
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Wacintosh
OPERATING SYSTEM: US/08/882,4
FILING DATE: June 25, 1997
CLASSIFICATION NUMBER: US/08/882,4
PILING DATE: June 25, 1997
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Moran, John
REGISTRATION NUMBER: 26,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Moran, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino Acid
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| Sequence 182, Application US/10428817A
| Publication No. US20040214783A1
| GENERAL INFORMATION:
| APPLICANT: TERMAN David S
| TITLE OF INVENTION:
| PILE REFERENCE: 38373-18918
| CURRENT APPLICATION NUMBER: US/10/428,817A
| CURRENT FILING DATE: 2003-05-05
| PRIOR APPLICATION NUMBER: US 60/378,988
| PRIOR APPLICATION NUMBER: US 60/309,366
| PRIOR APPLICATION NUMBER: US 60/406,697
| PRIOR PLING DATE: 2002-06-15
| PRIOR PLING DATE: 2002-08-28
| PRIOR PLING DATE: 2002-08-28
| PRIOR PLING DATE: 2002-08-29
| PRIOR PLING DATE: 2002-0-01
| PRIOR PLING DATE: 2002-0-01
| PRIOR PLING DATE: 2002-10-01
| PRIOR PLING DATE: 2002-10-01
| PRIOR PLING DATE: 2002-10-02
| PRIOR PLING DATE: 2002-10-02
| PRIOR PLING DATE: 2003-10-09
| PRIOR PLING DATE: 2003-10-09
| PRIOR PLING DATE: 2003-01-09
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  121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                      EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SEKSEEINEKDLARKKSELQGTA--GNKQIYYYNEKAKTENKESHDQFLQHTLLFKGFFTD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 991; DB 16;
80.3%; Pred. No. 2.6e-82;
tive 18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus
US-10-428-817A-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.0
Best Local Similarity 80.3
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                     SULT 26
-10-428-817A-182
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US-08-882-431-2
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SERVEMAL INFORMATION:

GENERAL INFORMATION:

CARDICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPERENCE: 38373-189118

CURRENT PELING DATE: 2003-05-05

PRIOR PELING DATE: 2002-06-08

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-29

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2003-01-02

PRIOR PILING DATE: 2003-01-02

PRIOR PILING DATE: 2003-01-03

PRIOR PILING DATE: 2003-01-03
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                                                                                                                                                                                                                                                                                                                                                                                                          60 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMY-GVTLHDNNRLT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHP
                                                                                                                                                                                                                                                       1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                      1 SEKSEBINEKDLARKKSBLQGAALGN-KQIYYYNEKAKTENKESHDQFLQHTLLFKGFFTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                   74.4%; Score 921; DB 18; Length 227; 79.4%; Pred. No. 6.3e-76; tive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 175, Application US/10428817A; Publication No. US20040214783A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus aureus
                              ; TYPE: PRT
; ORGANISM: Streptococcus aureus
US-10-997-690-11
                                                                                                                                         Query Match
Best Local Similarity 79.4%
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-428-817A-175
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LENGTH: 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.0%; Score 978; DB 8; Length 233; Best Local Similarity 79.3%; Pred. No. 4e-81; Matches 184; Conservative 17; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRASER, JOHN DAVID
APPLICANT: PROFT, THOMAS
TITLE OF INVENTION: SUPERANTICENS
TITLE REPERENCE: 12669-004001
CURRENT APPLICATION NUMBER: US/10/997,690
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 09/869,136
PRIOR PILING DATE: 1999-12-24
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTERO for Windows Version 4.0
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10997690 Publication No. US20050153376A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAK: (301) 619-7714
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOCEAN, JOHN
REGISTRATION NUMBER: 26,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Peptide
   FORT DETRICK
                              MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
US-10-997-690-11
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Sequence 10, Application US/10428817A

Sequence 10, Application US/10428817A

Sequence 11, Application No. US20040214783A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFRENCE: 38373-18918

FILE REFRENCE: 2003-05-05

FRIOR PAPLICATION NUMBER: US 60/378,986

FRIOR PAPLICATION NUMBER: US 60/389,366

FRIOR APPLICATION NUMBER: US 60/406,697

FRIOR PELING DATE: 2002-08-29

FRIOR PELING DATE: 2002-08-29

FRIOR PELING DATE: 2002-10-01

FRIOR PELING DATE: 2002-10-02

FRIOR PELING DATE: 2002-10-02

FRIOR PELING DATE: 2003-10-03

FRIOR PELING DATE: 2003-10-03

FRIOR PELING DATE: 2003-10-03

FRIOR PELING DATE: 2003-01-09

FRIOR PELING DATE: 2003-01-09
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                                                                                                                        S LINFEDLLINFNSKEMAQHFKSKAVDVYPIRYSINCYGGBIDRTACTYGGVTPHEGNKLK 145
                                                                                                                                                                                                                                                                                     86 LINFEDLLINFNSKEMAQHFKSKNVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNKLK 145
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                                                                              61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                       EEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 NENIDSVKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTD 85
26 NENIDSVKEKELHKKKSELSSTALNNMKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          206 RGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
US-10-428-817A-187
US-10-428-817A-187
Sequence 187, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-428-817A-10
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US-09-751-708A-14

Sequence 14, Application US/09751708A

Sequence 14, Application US/09751708A

Sequence 14, Application US/20030157113A1

SEQUENCE 10 
                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2000-01-14
FRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3:1
LENGTH: 258
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                                         LIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 258;
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Best Local Similarity 54.5%; Pred. No. 3e-52;
Matches 126; Conservative 35; Mismatches 70; Indels
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US-09-870-759-14
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RESULT 37
US-10-002-784A-34
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TILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE OF TATON NUMBER: US/10/428,817A

CURRENT APPLICATION NUMBER: US/0/389,366

PRIOR PILING DATE: 2002-06-08

PRIOR PILING DATE: 2002-06-15

PRIOR PELING DATE: 2002-00-01

PRIOR PELING DATE: 2002-10-01

PRIOR PELING DATE: 2002-10-01

PRIOR PELING DATE: 2002-10-02

PRIOR PELING DATE: 2003-01-09
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; Sequence 14, Application US/10937758A
; Sequence 14, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
    APPLICANT: TERMAN, David S
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
    CURRENT PILING DATE: 2004-09-08
    CURRENT PILING DATE: 2004-09-08
    PRIOR PILING DATE: 2004-08-30
    NUMBER OF SEQ ID NOS: 121
    SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14

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CRGANISM: Staphylococcus aureus
US-10-937-758A-14
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; ORGANISM: Staphylococcus aureus
US-10-428-817A-187
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 187
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Best Local Similarity 54.5%;
Matches 126; Conservative 3
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Best Local Similarity 54.5%
Matches 126; Conservative
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1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60

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72 GSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
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                                                                                                                                                                   121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
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APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: MALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                         20;
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TITLE OF INVENTION: Bacterial Superantigen Vaccines FILE REFERENCE: 033/23/5AP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT PILLING DATE: 2001-11-26
PRIOR PLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.2%; Score 523; DB 10;
Best Local Similarity 49.5%; Pred. No. 1.4e-39;
Matches 109; Conservative 25; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09900766; Publication No. US20030039655A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IENGTH: 203
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Challes H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
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                                                                                                                                                                                                                                                                                                                                 APLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ 1D NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SOTUMBER: Apple Macintosh Microsoft Word 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 399; DB 14;
Pred. No. 9.2e-29;
4; Mismatches 7;
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APPLICATION NUMBER: US/08/882,431B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: staphylococcal enterotoxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                    Sequence 32, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                   61 KTACMYGGVTLHDNNRLTEEKK 82
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Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                           103 KTACMYGGVTLHDNNRLTEEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.2%;
86.6%;
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Best Local Similarity 86.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                   US-10-002-784A-32
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CORRESPONDENCE ADDRESS:
ADDRESSES:
STREET: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                         43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                                                                                                                                                                                                                                                                                                 1 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 60
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                                                                                                                                                                                            36.9%; Score 457; DB 14; Length 82;
100.0%; Pred. No. 4.6e-34;
iive 0; Mismatches 0; Indels
                                                                                          FEATURE:
, OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORDY disk

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh

OFFRATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/767,687

FILING DATE: 29-Jan-2004

CLASSIFICATION: -UNKNOWN>

PRIOR APPLICATION: -UNKNOWN>

PRIOR APPLICATION WUMBER: US/08/882,431B

RILING DATE: June 25, 1997

ATTORNEY/AGRY INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19
                                             TYPE: PRT ORGANISM: staphylococcal enterotoxin E
                                                                                                                                                                                                                                                                                                                                                                                        103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                            61 KTACMYGGVTLHDNNRLTEEKK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10767687
Publication No. US2085064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-767-687-19
  SEQ ID NO 34
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43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102

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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173
                            JS-10-428-817A-173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: ANTONSSON, PER
APPLICANT: ANTONSSON, PER
APPLICANT: ANALSE, BOORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: PO2188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.2%; Score 399; DB 17; Length 8; Best Local Similarity 86.6%; Pred. No. 9.2e-29; Matches 71; Conservative 4; Mismatches 7; Indels
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29.6%; Score 366; DB 10;
Best Local Similarity 37.9%; Pred. No. 3.4e-25;
Matches 85; Conservative 46; Mismatches 81;
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
RAGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
                                                                                                                                                                                                                                  TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KTACMYGGVTLHDNNRLTEEKK 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Staphylococcus sp. US-09-900-766-6
                                                                                                                                                                                                                                                                                                                                            US-10-767-687-17
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US-09-900-766-6
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US-110-420-81/A-1/A

Sequence 173, Application US/10428817A

Publication No. US20040214783A1

GENERAL INFORMATION:

APPLICANT: TERVAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPREBRUCE: 38373-18918

CURRENT FILING DATE: 2003-05-05

PRIOR PRILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: US 60/318,988

PRIOR FILING DATE: 2002-06-08

PRIOR PRILING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR PLING DATE: 2002-06-18

PRIOR PLING DATE: 2002-08-29

PRIOR PLING DATE: 2002-08-29

PRIOR PLING DATE: 2002-08-09

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-02

PRIOR PLING DATE: 2002-10-03

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-02

PRIOR PLING DATE: 2002-10-03

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-02

PRIOR PLING DATE: 2002-10-01

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US-10-474-792-416

US-10-474-792-416

US-10-474-792-416

Publication No. US20040236072A1

GENERAL INFORMATION

APPLICANT: Olmsted, Stephen

APPLICANT: Nickbarg, Bliot

APPLICANT: Nickbarg, Bliot

APPLICANT: Nickbarg, Bliot

TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES

FILE REPRENCE: AN 100399

CURRENT APPLICANT: WINDER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: US/10/474,792

SOFTWARE: PatentIn version 3.0

SEQ ID NO 416

LENGTH: 259
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Sequence 177. Application US/10428817A

Dublication No. US20040214783A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INFORMATION:

PRICE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-09

PRIOR APPLICATION NUMBER: US 60/389,366

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2003-10-09

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Sequence 178, Application US/10428817A

Sequence 178, Application US/10428817A

Sequence 178, Application NO. US20040214783A1

SENERAL INFORMATION: US20040214783A1

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR FILING DATE: 2002-08-28

PRIOR FILING DATE: 2002-08-28

PRIOR FILING DATE: 2002-08-28

PRIOR FILING DATE: 2002-08-28

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 2002-08-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-177
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Publication No. US20040214783A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

CURRENT PILL NEPRANCION NUMBER: US/10/428,817A

CURRENT PAPLICATION NUMBER: US 60/378,988

PRIOR PAPLICATION NUMBER: US 60/378,988

PRIOR PAPLICATION NUMBER: US 60/389,366

PRIOR PAPLICATION NUMBER: US 60/389,366

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR PILING DATE: 2002-08-28

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-03

PRIOR PILING DATE: 2002-10-03

PRIOR PILING DATE: 2003-10-03

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 KDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ---KQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK------VQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN 78
                                                                                                                                                                                                                 34 EMSSVGVINLRNLYSTYDPTEVKGKINEGPPFSGSLFYKNI ----PYGNSSIELKVELNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYN----DLLVDLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 259;
                                                                                  84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
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27.7%; Score 343.5; DB 16
34.1%; Pred. No. 4.9e-23;
tive 44; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
                                                                                  Conservative
Query Match
Best Local Similarity
Matches 78; Conserv
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GENERAL INFUGATION:
GENERAL INFUGATION:
GENERAL INFUGATION:
COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US 60/318,988
FRIOR PELING DATE: 2002-05-08
FRIOR PELING DATE: 2002-06-08
FRIOR PELING DATE: 2002-06-15
FRIOR PELING DATE: 2002-06-29
FRIOR APPLICATION NUMBER: US 60/406,697
FRIOR FILING DATE: 2002-00-0
FRIOR PELING DATE: 2002-10-01
FRIOR PELING DATE: 2002-10-01
FRIOR PELING DATE: 2002-10-02
FRIOR APPLICATION NUMBER: US 60/415,400
FRIOR APPLICATION NUMBER: US 60/438,686
FRIOR APPLICATION NUMBER: US 60/438,686
FRIOR APPLICATION NUMBER: US 60/438,686
FRIOR FILING DATE: 2003-01-09
FRIOR APPLICATION NUMBER: US 60/438,686
FRIOR APPLICATION NUMBER: US 60/438,6
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                                                                                              ---SDSFGGKVQRGL 183
                                                             81 KGK-----KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 242;
                                                                                                                                                                                                                                                                                                                184 IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.0%; Score 310; DB 16; Best Local Similarity 33.2%; Pred. No. 5.2e-20; Matches 74; Conservative 39; Mismatches 76;
                                                                                                                                                                                     136 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 176, Application US/10428817A; Publication No. US20040214783A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09870759; Patent No. US20020177551A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-176
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US-10-428-817A-176
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FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT APPLICATION NUMBER: US 60/378,988
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR PILING DATE: 2002-05-08
PRIOR PELING DATE: 2002-06-15
PRIOR PELING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-29
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 2003-01-09
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEC ID NOS: 224
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEC ID NOS: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQTTVPIDK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAVDVYGLSYSGYCL----KNKYIYGGVTL-AGDYLEKSRRIPINLWVNGEHQTISTDK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGKVQRGLIVFHSSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 NLRQIYYYNBKAITENK--ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%; Score 320; DB 16; Length 239; 33.0%; Pred. No. 6.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
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   PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 178
LENGTH: 239
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US-10-428-817A-172
                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Conservative
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Best Local Similarity
Matches 76; Conserva
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Best Local Similarity
Matches 72; Conserv
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TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE;

FILE REPERENCE: 38373-18918

FILE REPERENCE: 38373-18918

CURRENT FILING DATE: 2002-05-05

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-06

PRIOR PELING DATE: 2002-06-15

PRIOR PELLING DATE: 2002-06-15

PRIOR PELLING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-29

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PRIOR FILING DATE: 2002-00-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-10-03

PRIOR FILING DATE: 2003-10-03

PRIOR FILING DATE: 2003-10-03

PRIOR FILING DATE: 2003-10-09

PRIOR FILING DATE: 2003-10-09

PRIOR FILING DATE: 2003-10-09

PRIOR FILING DATE: 2003-10-09
       203 BFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEV 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 LGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYQCYFSKKTNDINSHQTDKRKTCMYGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
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8-10-37-758A-10
; Sequence 10, Application US/10937758A
; Publication No. US20050112141A1
                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : PatentIn version 3.2
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hes 82; Conserva
                                                                                                                                                                      229 YLYT 232
                                                                                                                                                                                                                    260 YLTT 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pate
SEQ ID NO 6
LENGTH: 266
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US-09-751-708A-10
s Gequence 10, Application US/09751708A
s Sequence 10, Application US/09751708A
s Fublication No. US20030157113A1
s GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
CURRENT PELING DATE: 2002-10-15
PRIOR PAPLICATION NUMBER: US 60/173,371
PRIOR PLING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 266
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PATENTIN VEXBION 3.1
ENGTH: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                      24.3%; Score 300.5; DB 9; 33.6%; Pred. No. 4.4e-19; tive 47; Mismatches 96;
                                                                                                                                                                                                                                                                                  ; ORGANISM: Staphylococcus aureus
US-09-870-759-10
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Best Local Similarity 33.68
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 YLYT 232
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GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REFERENCE: 38373-189118
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                                                                                                                                                                                                                                                                                                                                                                                                          15 SMESOPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDOFLYFDLIYSIKDTK 73
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                                                                                                                                                                                                                                                                            Length 255;
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REFERENCE/DOCKET NUMBER: 2879-29-C1
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CURRENT PELLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR PILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR PILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-00-01
PRIOR FILING DATE: 2002-00-10
PRIOR FILING DATE: 2002-00-10
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOCTWARE: PAECHIN VERSION 3.2
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Mismatches
                                                                                                                                                 TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183, Application US/10428817A
Publication No. US20040214783A1
                                           (303) 863-9700
                      TELECOMMUNICATION INFORMATION
                                                        TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
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nes 83; Conservative
                                         TELEPHONE:
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Matches 82; Conserv
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      APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: FILE REFERENCE 650884
CURRENT APPLICATION NUMBER: US/10/937,758A
CURRENT FILING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/650,884
PRIOR PILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN VEXESION 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC------AGGTPNKTACMYGG 110
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Publication No. US20030202962A1
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
Elmslie, Robyn B.
POTTLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                 ; Score 300.5; DB 1'; Pred. No. 4.4e-19; 47; Mismatches 96
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FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/580,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Connell, Gary J
                                                                                                                                                                                                                                                                                   , ORGANISM: Staphylococcus aureus
US-10-937-758A-10
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24.3%;
Best Local Similarity 33.6%;
Matches 82; Conservative 4'
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STATE: Colorado
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US-10-354-948-2
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                                                                                                                                                                                                                                                               TYPE: PRT
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                     1 ESQPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
EKSEEINEKDLRKKSELORNALSNLROIYYYNEKAITENKESDDOFLENTLLFKGFFTGH
                                                              --- AGGTPNKTACMYGGV
                                                                                                                                                                                      172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Arad, Gila
APPLICANT: Arad, Gila
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
TITLE OF INVENTION: ANTAGONISTS AND VACCINES
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1996-09-10
PRIOR FILING DATE: 1997-12-30
PRIOR FILING DATE: 1997-12-30
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                            62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC--
                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09150947B Patent No. US20020028211A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus aureus US-09-150-947B-12
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LENGTH: 239
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Matches
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RESULT 56 US-10-172-425B-12

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Sequence 163, Application US/10428817A

Publication No. US20040214783A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT FILING DATE: 2003-05-06

PRIOR PELING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: US 60/389,366

PRIOR PILING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PELING DATE: 2002-08-28

PRIOR PELING DATE: 2002-08-28

PRIOR PELING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 60/415,310

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-02

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 239;
                                                                                                                                                               TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
CURRENT APPLICATION NUMBER: US/10/172,4258
CURRENT FILING DATE: 2002-06-13
FRIOR APPLICATION NUMBER: 09/150,947
FRIOR FILING DATE: 1998-09-10
FRIOR FILING DATE: 1998-09-10
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1996-12-30
FRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.2%; Score 299.5; DB 1
33.7%; Pred. No. 4.7e-19;
tive 46; Mismatches 96
Sequence 12, Application US/10172425B Publication No. US20030147908A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 224

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US-09-308-830-13
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APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Manuela
APPLICANT: Scoehr, Jonanier
APPLICANT: Stochr, Jonanier
APPLICANT: Ohlendorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REPERENCE: 600.31105W0
CURRENT APPLICATION NUMBER: US/08/973,391A
CURRENT FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: US 08/480,261
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
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                                                                                                                               DB 16; Length 251;
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es 92; Indels
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                                                                                                                                                                  45; Mismatches
                                                                                                                             Score 295.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08973391A Publication No. US20020054887A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes
                                                                       ORGANISM: Streptococcus pyogenes
SOFTWARE: Patentin version 3.2
SEQ ID NO 163
LENGTH: 251
                                                                                                                           ch 23.9%;
l Similarity 34.2%;
81; Conservative 45
                                                                                                                               Query Match
Best Local Similarity
Matches 81; Conserv
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                                                          TYPE: PRT
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Sequence 13, Application US/09308830
Publication No. US20020086813A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                 CCMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/308,830
FILING DATE: 04-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.8%; Score 294.5; DB 9; Best Local Similarity 34.2%; Pred. No. 1.4e-18; Matches 81; Conservative 45; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 600.346USWO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US97/22228
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: 60/032,930
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant & Gould P.C.
STREET: P.O. Box 2903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                  ZIP: 55402-0903
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                           JAPELCANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REPERBUES: 1213-6.1USMO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
FRIOR PELING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-01
PRIOR PILING DATE: 1999-12-01
PRIOR PILING DATE: 1999-12-01
PRIOR PILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 4
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DLHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVXT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDOFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GapB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.7%; Score 293.5; DB 17; Length 240; Best Local Similarity 33.3%; Pred. No. 1.7e-18; Matches 78; Conservative 48; Mismatches 89; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 293.5; DB 14; Length 266; 32.8%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2010.11-26
PRIOR APPLICATION NUMBER: 08/882,431, 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 6
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: mutant staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: MISC_FEATURE
; LOCATION: (240)...(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-4
                  Sequence 4, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-10-002-784A-6
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CORRESPONDENČE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
7;
                                                                                                                      61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
                                                                                                                                                  111 VTLHDNNRLTEEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                            171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                             27 AESQPDPKPDELHKSSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
                                        1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  Gaps
  19;
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45; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: 
UNKNOWN>

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TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-767-687-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (301) 619-7714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6
  80; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      229 YLYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
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                                                                      110
                                                                                             VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                  171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                            203 BFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMMYNDNKAVDSKDVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
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9
                                 27 AESQPDPKPDELHKSSKP--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
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                                                                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mason, Hugh
APPLICANT: Palmer, Kenneth
APPLICANT: Palmer, Kenneth
APPLICANT: Palmer, Kathleen
APPLICANT: Mor, Tagfrir
APPLICANT: Mor, Tagfrir
APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
FILE REPERENCE: 486,94453
CURRENT APPLICATION NUMBER: US/10/151,336
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10151336
Publication No. US20030079248A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: bean yellow dwarf virus
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                                                                                                                                                                                                                                                                                                    229 YLYT 232
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RESULT 64 US-08-882-431-16

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SEE: John Moran
: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
FORT DETRICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TEEKKVPINLMIDGKOTTVPIDKVKTSKKEVTVQELDLOARHYLHGKFGLYNSDSFGGKV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYBGDPVTHENVKSVDQLRSHDLIYN---VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.4%; Score 289.5; DB 8; Best Local Similarity 33.8%; Pred. No. 4.1e-18; Matches 80; Conservative 45; Mismatches 93;
                                                                                                                                    TITLE OF INVENTION: Bacterial Superantigen TITLE OF INVENTION: Vaccines UNDBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.5 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/882,431 FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 65
US-10-002-784A-16
Sequence 16, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
lence 16, Application US/088B2431
lication No. US20030009015A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Moran, John REGISTRATION NUMBER: 26,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                             APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino Acid
                                                                                                                                                                                                                                                                                               STATE: MARYLAND COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       21702-5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 TEEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VDLGSKDATNKYKGKKVVDLYGAYYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 LTEEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 LDKYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFNN--SP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65
                                                                                                                                                                                                                                                                                                                                                         4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KKSELORNA-----LSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTGHPWYNDLL
                                                                                                                                                                                                                                                                                                                                                                                                     25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 YETGYIKFIENENS-FWYDWMPAPGDKFDQSKYLMMYNDNKMYDSKDVKIEVYLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VORGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic US-10-002-784A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.3%; Score 288.5; DB 14; Length Best Local Similarity 33.9%; Pred. No. 4.8e-18; Matches 80; Conservative 45; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                        93; Indele
                                                                                                                                                                                                                                                      DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REPERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                      ; Score 289.5; DB 1'; Pred. No. 4.1e-18; 45; Mismatches 93.
                                                                                                  STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-002-784A-10
. Sequence 10, Application US/10002784A
. Publication No. US20030036644A1
. GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 16:
                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      23.4%;
33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 10
LENGTH: 239
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                        80; Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                     US-10-767-687-16
                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 EIPKKIVVKVSIDGIQ-SLSPD-IETNKKAVTAQELDYKVRKYLTDNKQLYTNGP--SKY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 GPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 ETGYİKFIPKNKESFWFDFFPEPEFTQSKY----LMİYKDNETLDSNTSQİEVYLTT 250
                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 251;
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.4%; Score 289.5; DB 1.
Best Local Similarity 33.8%; Pred. No. 4.1e-18;
Matches 80; Conservative 45; Mismatches 93
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 21702-5012
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                  US-10-002-784A-16
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                                                                                                                                                                             SEQ ID NO 16
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Heblication No. US20050026272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US/09/555,115
PRIOR APPLICATION NUMBER: US/09/555,115
PRIOR PILING DATE: 2000-08-20
PRIOR PILING DATE: 1998-12-01
PRIOR PILING DATE: 1998-12-01
PRIOR PILING DATE: 1999-12-01
PRIOR PILING DATE: 1999-12-01
PRIOR PILING DATE: 1999-12-01
SROFTHARE: PALEGATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1999-12-01
SROFTHARE: PALEGATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1999-12-01
SROFTHARE: PALEGATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR PILING DATE: 1999-12-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 --KKVPINLMIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 DLHKSSER-TGTMGNMK--YLYDDHYVSATKVKSVDKELAHDLIYNISDKKLKNYDKVKT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 DLRKKSELORNALSNIRQIYYYNEKAITENK-ESDDOFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 TGYIKFIENNGNIFQYDMMPAPGDKFDQSKYLAMYNDNKTVDSKSVKIEVHLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.3%; Score 288.5; DB 17; Length Best Local Similarity 32.1%; Pred. No. 4.8e-18; Matches 75; Conservative 49; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (240)
COTHER INFORMATION: Xaa is unknown.
US-10-923-324-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: J
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VDLGSKDATNKYKGKKVDLYGAYYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KKSELQRNA----LSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 VQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
23.3%; Score 288.5; DB 17; Length 239;
Best Local Similarity 33.9%; Pred. No. 4.8e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23;
                                                                                                                                                                 Sequence 10, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION:
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION MARBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKNOWN>
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA: Woll 10.10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
WOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: (301) 619-2065
(301) 619-7714
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 69
US-10-923-324-3
; Sequence 3, Application US/10923324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-767-687-10
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70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
10 DLHKSSEF-TGTMGNMK--YLYDDDHYVSATKVKSVDKFLAHDLIYNISDKRLKAYDKVKT 66
                                                                                                                                                                                                                   181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 1213-1.USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
FRIOR APPLICATION NUMBER: US/09/555,115
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR PILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR PILING DATE: 1999-12-01
PRIOR PILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VDLGSKDATNKYKGKKVDLYGAYYGYQCAGG------TPNKTACMYGGVTLHDNNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 LTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 KKSELQRNA----LSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KPDELHKSSKFTGKMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.2%; Score 287.5; DB 8; Length 239; Best Local Similarity 33.9%; Pred. No. 5.9e-18; Matches 80; Conservative 45; Mismatches 88; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.2%; Score 287.5; DB 1 Best Local Similarity 32.1%; Pred. No. 5.9e-18; Matches 75; Conservative 48; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , NAME/KEY: MISC_FEATURE
; LOCATION: (240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-6
                                                        ATTORNEY AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
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ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Peptide
      PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                              STRANDEDNESS: Unkr
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                         US-08-882-431-10
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11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69

92; Indels 19;

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Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; Publication No. US20050026272A1
; Publication No. US20050026272A1
; Publication No. US2005002627A1
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136_1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT APPLICATION NUMBER: US/09/555,115
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR PILING DATE: 1990-12-01
; PRIOR PILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EKSEEINEKDLRKKSELORNALSNIRQIYYYNEKAITENK-ESDDOFLENTLLFKGFFTG
183 TGYIKFIENNGNTFQYDMMPAPGDKFDQSKYLAMYNDNKTVDSKRVKIEVHLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.1%; Score 285.5; DB 17; Length Best Local Similarity 31.3%; Pred. No. 9e-18; Matches 76; Conservative 49; Mismatches 99; Indels
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2-10-428-817A-186
; Sequence 186, Application US/10428817A
; Publication No. US20040214783A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (240)
OTHER INFORMATION: Xaa is unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic US-10-002-784A-8
                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 266;
                                                                                                       Length 240;
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                                                                                                 22.9%; Score 283.5; DB 17; Length 31.3%; Pred. No. 1.4e-17; ive 49; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APJICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 8
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
i LOCATION: (240)...(240)i OTHER INFORMATION: Xaa is unknown.
US-10-923-324-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                    Query Match
Best Local Similarity 31.31
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 LYT 232
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                      GARRANT INFORMATION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE: 3837-189118
CURRENT APPLICATION NUMBER: US 60/378, 988
RIOR FILING DATE: 2002-05-08
PRIOR PELING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR PELING DATE: 2002-10-02
PRIOR PELING DATE: 2003-01-09
PRIOR PELING DATE: 2003-01-09
PRIOR PELING DATE: 2003-01-09
PRIOR PELING DATE: 2003-01-09
PRIOR PELING DATE: 2003-01-09
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Publication No. US20050026272A1

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USWO

CURRENT APPLICATION NUMBER: US/09/555,115

PRIOR APPLICATION NUMBER: US/09/555,115

PRIOR FILING DATE: 1998-12-01

PRIOR FILING DATE: 1998-12-01

PRIOR FILING DATE: 1998-12-01

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 2

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGIPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%; Score 285.5; DB 16; Length 266; 32.1%; Pred. No. 1e-17; Live 49; Mismatches 91; IndelB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75; Conservative
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NAME/KEY: MISC_FEATURE
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Best Local Similarity
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Sequence 6, Application US/0882431
Fublication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Mark A. Olson
APPLICANT: Mark A. Olson
ITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
INUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Mismatches
                                                                                                                                                  Application US/10428817A
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ORGANISM: Staphylococcus aureus
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Best Local Similarity
Then 76; Conserva
   260 YLTT 263
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LENGTH: 239
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ADDRESSE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
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Best Local Similarity 32.8%; Pred. No. 1.9e-17;
Matches 80; Conservative 46; Mismatches 99
                                                                                                                                                                       Sequence 8, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/767,687
FILING DATE: 29-Uan-2004
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/882,431B
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STRANDEDNESS: Unknown
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-767-687-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
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260 YLTT 263
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GENERAL INFORMATION:

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APPLICATION NO. US20050026272A1

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USWO

CURRENT APPLICATION NUMBER: US/10/923,324

CURRENT APPLICATION NUMBER: US/09/555,115

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 8

LENGT: 1240
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                                                                                                                                                                                                                                                                                            Length 240;
                                                                                                                                                                                                                                                                                            22.3%; Score 276.5; DB 17; Length 30.5%; Pred. No. 6e-17; ive 52; Mismatches 98; Indels
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LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
                                                                                                                                                                              NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
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                                                                                        LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.5
Matches 74; Conservative
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    : US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
FORT DETRICK
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Publication No. US20050026272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bobach, Geregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US/09/555,115
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 1998-12-01
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.6%; Score 280; DB 8; Length 265
Best Local Similarity 31.6%; Pred. No. 3.3e-17;
Matches 77; Conservative 45; Mismatches 102; Indels
                                                                                          ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOXAN. JOHN
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
                                                   MARYLAND
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US-10-923-324-7
                                                                          COUNTRY:
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FILE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US (0/378,988

PRIOR APPLICATION NUMBER: US (0/378,988

PRIOR APPLICATION NUMBER: US (0/389,366

PRIOR APPLICATION NUMBER: US (0/389,366

PRIOR PILING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PELING DATE: 2002-06-15

PRIOR PILING DATE: 2002-08-28

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-10-01

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PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2003-10-02

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PRIOR PILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 NDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN----KTACMYGGVTLHDNNRL 119
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171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TEEKKVPINLWI---DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                     35 EQLN-----KSSQFTGVMGNLRCL-YDNHFVEGTNVRSTGQLLQHDLIFPIKDLKLKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 DSVKTEFNSKDLAAKYKNKDVDIFGSNYYYNCYYSEGNSCKNAKKTCMYGGVTEHHRNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 BEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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21.6%; Score 267.5; DB 16; Length
Best Local Similarity 33.1%; Pred. No. 4.4e-16;
Matches 78; Conservative 37; Mismatches 98; Indels
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; Patent No. US20020177551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                          229 YLYT 232
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US-09-870-759-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: John Moran
STREET: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGG------TPNKTACMYGG 110
                                                               172 SDSFGGKVORGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                         114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert G. Ulrich,
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 21702-5612
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macincosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/882,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Moran, John
REGISTRATION UNMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 619-2065
TELEPAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION NOWBER: US/08/
FILING DATE: June 25, 1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.0
Matches 78; Conservative
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STRANDEDNESS: Un
                                                                                                                                                                                                                                                                                                                                                                 230 LYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                  234 LTT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 81
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CAMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERRENCE: 38373-189118
CURRENT APPLICATION NUMBER: US 60/318,988
FRICA PAPLICATION NUMBER: US 60/318,986
FRICA FILING DATE: 2002-06-08
FRICA PAPLICATION NUMBER: US 60/389,366
FRICA RELING DATE: 2002-06-29
FRICA REPLICATION NUMBER: US 60/406,697
FRICA RELING DATE: 2002-08-28
FRICA RELING DATE: 2002-08-29
FRICA RELING DATE: 2002-10-01
FRICA RELING DATE: 2002-10-01
FRICA RELING DATE: 2002-10-02
FRICA RELING DATE: 2002-10-02
FRICA RELING DATE: 2003-10-09
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                                                                                                                              203 FNS--SPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLAMYNDNKTVDSKSVKIEVH 260
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114 HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKKBVTVQELDLQARHYLHGKFGLXN 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL
                                                                                                           172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 86
US-10-937-758A-12
; Sequence 12, Application US/10937758A
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Conservative
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Best Local Similarity
Matches 74; Conserva
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                                                                                                                                                                                                              230 LYT 232
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                      APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REFERENCE: 970759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
LENGTH: 266
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Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPRENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR PELING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                               21.5%; Score 266.5; DB 9; Length 266; 30.5%; Pred. No. 5.6e-16; ative 51; Mismatches 101; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 266;
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                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus aureus US-09-870-759-12
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Best Local Similarity
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           SENERAL INFORMATION:
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US-09-751-708A-12
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LENGTH: 266
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Best Local
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ADDRESSEE: John Moran
STREET: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                               62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLH 114
                                                                                                                                           59 KNYDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKH 118
                                                                                                                                                                                                      115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNS 172
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                                               173 DSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08882431
Publication No. US2003009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: SIMB Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCES: John Moran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/882,431
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SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
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TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                   APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: FILE REFERENCE 650884
CURRENT APPLICATION NUMBER: US/10/937,758A
CURRENT FILING DATE: 2004-09-08
PRIOR PILIATION NUMBER: 09/650,884
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
LENGTH: 266
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TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REPERENCE: 1213-6-1USM
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
FRIOR PAPLICATION NUMBER: US/09/555,115
PRIOR PAPLICATION NUMBER: PCT/US98/25107
PRIOR PILING DATE: 1998-12-01
PRIOR PILING DATE: 1998-12-01
PRIOR PAPLICATION NUMBER: US 60/067,357
PRIOR PILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PARCENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                          Score 266.5; DB 1
Pred. No. 5.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
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OTHER INFORMATION: Xaa is unknown
                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-12
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ORGANISM: Staphylococcus aureus
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Best Local Similarity 30.5%;
Matches 74; Conservative 5
Publication No. US20050112141A1
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Best Local Similarity 30.69
Matches 74; Conservative
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                     GENERAL INFORMATION
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RESULT 91
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                                                                  114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                               172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                          61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SEKSEEINEKDIRKKSELQRNALSNIRQIYYYNEKAITENKESDDOFLENTLIFKGFFTG 60
172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.9%; Score 258.5; DB 14; Length 266; 30.0%; Pred. No. 3e-15; ive 51; Mismatches 102; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/213/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 146
LERGTH: 266
                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
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US-10-767-687-14
; Sequence 14, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 LYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 LTT 263
                                                                                                                                                                                                                                          230 LYT 232
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US-10-002-784A-14
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CORRESPONDENCE ADDRESS:
ADDRESSER: Carles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114. HONNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEKSBEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.9%; Score 258.5; DB 17;
30.0%; Pred. No. 3e-15;
tive 51; Mismatches 102;
                                                                   TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (301) 619-7714
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 30.0
Matches 73; Conservative
                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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110 GVTLHDNNRLTBEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 LVTKKLDVRDARDFFINSEMDEYAANDFKTGDKIAVFSVPFDWNYLSKG---KVTAYTYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 210;
                                                                                                              192 STVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 20.7%; Score 256; DB 16; I Similarity 27.4%; Pred. No. 3.8e-15; 66; Conservative 51; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10997690 Publication No. US20050153376A1 GENERAL INFORMATION:
APPLICANT: FRASER, JOHN DAVID APPLICANT: PROFT, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-10-997-690-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 SELORNAL-SNLRQIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTGHPWYNDLLVDLG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLHRSSLVKNLONIYFLYEGDPVTHENVKSVDOLRSHDLIYN---VSGPNYDKLKTELK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.7%; Score 256.5; DB 14; Length 468; Best Local Similarity 33.8%; Pred. No. 9.7e-15; Matches 76; Conservative 43; Mismatches 85; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.7%; Score 256.5; DB 14; Length 220; Best Local Similarity 33.8%; Pred. No. 3.6e-15; Matches 76; Conservative 43; Mismatches 85; Indels 21;
                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFWFDFFPBPBFFTQSKY----LMIXKDNETLDS-NTQIEVYLTT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 STVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APJICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 27:
LENGTH: 468
TITLE OF INVENTION: Bacterial Superantigen Vaccines FILE REFERENCE: 003/233/SAP CURRENT APPLICATION NUMBER: US/10/002,784A CURRENT FILING DATE: 201-11-26 PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776 PRIOR FILING DATE: 97-06-25; 98-09-01 NUMBER OF SEQ ID NOS: 40 SOFTWARE Apple Macintosh Microsoft Word 6.0 SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion US-10-002-784A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
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US-10-428-17A-17D

US-10-428-17A-17D

Sequence 170, Application US/10428817A

Publication No. US20040214783A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT APPLICATION NUMBER: US 60/318,988

PRIOR PILING DATE: 2002-06-05

PRIOR PELING DATE: 2002-06-15

PRIOR PLING DATE: 2002-06-15

PRIOR PLING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR PLING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR APPLICATION NUMBER: US 60/415,310

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-02

PRIOR PPLICATION NUMBER: US 60/415,310

PRIOR PLING DATE: 2003-10-09

PRIOR PLING DATE: 2003-10-09

PRIOR PLING DATE: 2003-10-09

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                                                                       132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
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Sequence 16, Application US/10428817A

Sequence 16, Application US/10428817A

Publication No. US20040214783A1

GENERAL INPORMATION:

APPLICANT: TERMAN, David S

TITLE OF INNENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 38373-189118

CURRENT FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/389,366

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR PILING DATE: 2002-08-28

PRIOR PILING DATE: 2002-08-28

PRIOR PLING DATE: 2002-08-28

PRIOR PLING DATE: 2002-08-28

PRIOR PLING DATE: 2002-08-28

PRIOR PLING DATE: 2002-08-29

PRIOR PLING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR PLING DATE: 2002-08-29

PRIOR PLING DATE: 2002-10-01

PRIOR PLING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR APPLICATION NUMBER: US 60/173,371
SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO COMPOSITION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 SIDGIQSLSFDIEQIKNG----NCSRISYTVRKYLTDNKQLYTNGP--SKYETGYIKFIP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 LKNQEMATLFKDKNVDIYGVEXYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 WIDGKQT-TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHS 188
                                                                                            152 SIDGIQSLSFDİEQIKNG----NCSRISYTVRKYLTDNKQLYTNGP--SKYETGYİKFIP 205
                                                    130 WIDGKQT-TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHS 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 LKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKV
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                                                                                                                                                                                206 KNKESFWFDFFPPFFTGSKY----LMIYKDNETLDSNTSQIEVYLTT 249
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                                                                                                                                                      189 SEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
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ORGANISM: Streptococcus pyogenes
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Best Local Similarity 30./*
Best Tocal Similarity 70; Conservative
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US-09-751-708A-20
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Sequence 20. Spplication US/09870759

Batent No. US20020177551A1

GENERAL INFORMATION:
APPLICANT TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REPERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT PILING DATE: 2002-01-14

CURRENT PILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: PatentIn version 3.1

SOFTWARE: PatentIn version 3.1

LENGTH: 250
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19.8%; Score 245; DB 9; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.7%; Score 256; DB 18; Sest Local Similarity 27.4%; Pred. No. 4.3e-15; Matches 66; Conservative 51; Mismatches 58;
                                                                                                         PRIOR APPLICATION NUMBER: 09/069,136
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 1090-112-24
PRIOR FILING DATE: 1999-112-24
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 2
                                  FILE REFERENCE: 12669-004001
CURRENT APPLICATION NUMBER: US/10/997,690
CURRENT FILING DATE: 2004-11-24
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             TITLE OF INVENTION: SUPERANTIGENS
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ORGANISM: Streptococcus pyogenes
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US-09-870-759-20
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPEBRICE: 38373-18918

FILE REPEBRICE: 38373-18918

CURRENT PELLOATION NUMBER: US 60/378,988

PRIOR PELLOATION NUMBER: US 60/378,988

PRIOR PELLOATION NUMBER: US 60/389,366

PRIOR PELLOATION NUMBER: US 60/389,366

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR PELLOATION NUMBER: US 60/406,697

PRIOR PELLOATION NUMBER: US 60/406,750

PRIOR FILING DATE: 2002-08-29

PRIOR PELLOATION NUMBER: US 60/415,310

PRIOR PELLOATION NUMBER: US 60/415,300

PRIOR PELLOATION NUMBER: US 60/415,400

PRIOR PELLOATION NUMBER: US 60/415,400

PRIOR PELLOATION NUMBER: US 60/415,400

PRIOR APPLICATION NUMBER: US 60/415,400

PRIOR PELLOATION NUMBER: US 60/415,400
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT PRILICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR PLING DATE: 2002-05-08
PRIOR PLLING DATE: 2002-05-08
PRIOR PLLING DATE: 2002-06-15
PRIOR PLLING DATE: 2002-06-15
PRIOR PLLING DATE: 2002-06-15
PRIOR PLING DATE: 2002-06-15
PRIOR PLING DATE: 2002-06-15
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Best Local Similarity 27.0%; Pred. No. 1.3e-13;
Matches 65; Conservative 48; Mismatches 62;
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                                                               Sequence 169, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus pyogenes US-10-428-817A-169
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| Sequence 20. Application US/1093758A
| Publication No. US20050112141A1
| Publication No. US20050112141A1
| GENERAL INFORMATION:
| APPLICANT: TERMAN, David S
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
| FILE REPERBNCE: FILE REFERENCE 65084
| CURRENT PILING DATE: 2004-09-08
| PRIOR PLING DATE: 2000-08-30
| NUMBER OF SEQ ID NOS: 121
| SEQ ID NO 20
| LENGTH: 250
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Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 2
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Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94;
                                  60/438,686
                                                                                                                                                                                                                                             ) ORGANISM: Streptococcus pyogenes
US-10-428-817A-16
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PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/4
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin version 3.2
SEQ ID NO 16
LENGTH: 250
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
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17.8%; Score 220.5; DB 16; Length 240;
Best Local Similarity 29.7%; Pred. No. 7.9e-12;
Matches 63; Conservative 42; Mismatches 92; Indels 15; Gaps
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PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR PELING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2003-01-09
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 184
LENGTH: 240
TYPE: PRT
CRANISM: Staphylococcus aureus
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: B. VIRUS TRANSMISSION
                                                                                                                                                                                                                                                   HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                               61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                      EBKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                         Gaps
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                                                                             Query Match 100.0%; Score 1238; DB 4; Length 233; Best Local Similarity 100.0%; Pred. No. 9.3e-119; Matches 233; Conservative 0; Mismatches 0; Indels 0.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: CCALLZZ, Laura & 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1909-9090
TELECOMMUNICATION 1909-9090
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STREET: 1155 Avenue of the Americas
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Patent No. 6013263
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
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ryPE: amino acid

syntymboness:

rOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-486-099-112
                 TYPE: peptide
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CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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US-08-695-692B-8
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APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                      84
                                                                                                                                   25 SEKSEEINEKOLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                   1 SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                     Gaps
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Score 1238; DB 3; Length 257;
Pred. No. 1.1e-118;
Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
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Pred. No. 1.1e-118;
  Query Match
100.0%; Score 1238; Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 233; Conservative 0; Mismatches
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PILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Remonds
STREET: 1155 Avenue of the Americas
CITY: New York
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(212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 122:
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85 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
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TITLE OF INVENTION: OF MEWBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
25 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 84
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APPLICATION NUMBER: US/08/919,597
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 112, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: BOLOGNESI, Dani P.
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Langlois, Alphonse J
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Matthews, Thomas J.
Wild, Carl T.
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
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TELEBHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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Lambert, Dennis M
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amino acid
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ZIP: 10036-2711
COMPUTER READABLE FORM:
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APPLICANT: Lambert, Dennis M.
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APPLICANT: Lamberton R.
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APPLICANT: Lamberton
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0; Gaps
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Pred. No. 1.1e-118;
; Mismatches 0;
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Pennie & Edmonds LLP
7: 1155 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112, Application US/08484223B Patent No. 6020459
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Matthews, Thomas J
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 233; Conservative
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-2238-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                       145 EEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                                                                                                                                                                                                                                                                                             APPLICANT: Balognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Sham O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis J.
TITLE OF INVENTION: WETHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
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                                                                                                                     205 RGLIVPHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLXLXTT 257
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 37,742
REFERENCE/POCKET NUMBER: 37,742
REFERENCE/POCKET NUMBER: 30,742
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1238; DB 3;
100.0%; Pred. No. 1.1e-118;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                            US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
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(212) 869-9741/8864
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
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LENGTH: 257 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                121 BEKKUPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                               HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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    SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LESSEE: Pennie & Edmonds LLP
EET: 1155 Avenue of the Americas
': New York
T: New York
'YR: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 112, Application US/08475668A
; Patent No. 6060065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPA: (212) 869-9741/8864
TELEX. 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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Matches 233; Conservative
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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205 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennia M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alephens J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION ASSOCIATED EVENTS, INCLUI
TITLE OF INVENTION: MESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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100.0%; Pred. No. 1.1e-118;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                               Sequence 112, Application US/08485264A Patent No. 6228983 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-9741/9864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
                                                                                                                                                                                                                                                                                                                                                    Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 233; Conservative
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STATE: New York
COUNTRY: USA
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                                                                                                                                    RESULT 9
US-08-485-264A-112
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STREET: 11
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                                                                                                                                                                                                                                                                                                                                          Sequence 112, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones R.
APPLICANT: Langlois, Alphones N.
APPLICANT: Langlois, Alphones R.
APPLICANT: Langlois, Alphones R.
APPLICANT: Langlois, Alphones R.
APPLICANT: Langlois, Alphones R.
APPLICANT: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
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                                                                                         205 RGLIVEHSSEGSTVSYDLFDAQQQYPDTLLRIYRDNKTINSENLHIDLYLYTT 257
                                          181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTLAZI, Laura A.
NAME: COTLAZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REGISTRATION STORY 100-9090
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
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MOLECULE TYPE: protein
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100.0%; Score 1238; DB 4;
100.0%; Pred. No. 1.1e-118;
iive 0; Mismatches 0;
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               Bolognesi, Dani P. Matthews, Thomas J.
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TELEX: 66141 PERNIB
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                        Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 257 amino acids
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Best Local Similarity 100.
Matches 233; Conservative
                                                                            Wild, Carl T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                               APPLICANT:
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Sequence 112, Application US/08474349A

Sequence 112, Application US/08474349A

Belent No. 6333395

GENERAL INFORMATION:

APPLICANT: Belognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITION FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: COMPOSITION FOR INCLUDING HUMAN PARAINFLUENCE

TITLE OF INVENTION: VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

CORRESPONDENCE NOW YORK

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COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BATCHILIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIPICATION:
ATTORNEY AGGNT INFORMATION:
NAME: COTIZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 112:
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amino acid
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Best Local Similarity 100.
Matches 233; Conservative
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MOLECULE TYPE: protein
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Sequence 112, Application US/08470896

RESULT 11 US-08-470-896-112

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APPLICANT: Petteway, Stephen R.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANB FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

TITLE OF INVENTION: TRANSMISSION

CORRESPONDENCE: 273

ADDRESSEE: Pennie & Edmonds
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CCAULZI, LAULER
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 37,792
TELEPONDE: COLORY OF THE COMPATION:
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Patent No. 6518013
GENERAL INFORMATION:
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APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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US-09-350-841A-1598
Sequence 1598, Application US/09350841A
Patent No. 675000B
GENERAL INFORMATION:
APPLICANT: Joff8, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: METALON-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
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                                                                                                                                                                        CONTEXT FOUNDERS:

CONTEXT: 1155 Avenue of the Americas
CITY: New York
STATE: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487, 266A
FILING DATE: O'-UNN 1995
CLASSIFICATION: 435
ATTONEY AGENT INPORMATION:
NAME: COLUZZ: Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
RELEPRANT OF THE TOWN NUMBER: 30,742
RELEPRANT CALL STATEMENT ON THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANT (212) 790-9090
TELEFRANT (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 233; Conservative
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                                             APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphone J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
WUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                  STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 112, Application US/08487266A
Patent No. 6824783
GENERAL INFORMATION:
APPLICANT: BOLOGNesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNER
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
Matthews, Thomas J
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TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 100.
Matches 233; Conservative
                         ild, Carl T
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                         APPLICANT:
APPLICANT:
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US-09-314-235-24
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                                                                                                           Length 254;
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                                                                                                                                                 Indels
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APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.6%; Score 1171; DB 3; Best Local Similarity 95.7%; Pred. No. 6.6e-112; Matches 220; Conservative 4; Mismatches 2;
                                                                                                           97.1%; Score 1202; DB 4;
98.3%; Pred. No. 5.2e-115;
cive 0; Mismatches 2;
                                     TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 24, Application US/08896933
; Patent No. 6221351
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                                                                                                           Query Match
Best Local Similarity 98.3<sup>1</sup>
Matches 230; Conservative
                                                                         US-09-350-841A-1598
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LENGTH: 226
SEQ ID NO 1598
                   LENGTH: 254
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; Sequence 24, Application US/09314235; Patent No. 6338845

RESULT 16 US-09-314-235-24

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64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1171; DB 4; Length 226; Pred. No. 6.6e-112;
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PARLICANT: CERTAIN DAVID S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE REPERRANCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT PILLING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER PLILING DATE: 1997-07-18
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-01
EARLIER FILING DATE: 1991-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
NUMBER OF SEQ ID NOS: 34
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US-09-708-008B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Staphylococcus aureas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.6%;
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Best Local Similarity
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US-09-708-008B-24
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wald, Carl T.
APPLICANT: Lambert, Denies J.
APPLICANT: Lambert, Denies J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
ATTORNEY/ACCURATION: 435
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I: 1155 Avenue of the Americas
New York
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                                                                                                                                                                                                                                                                                          Sequence 113, Application US/08486099
Patent No. 6013263
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                                                                                                                                                                                                                                                                                                                                                            Bolognesi, Dani P.
Matthews, Thomas J
Wild, Carl T.
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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amino acid
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LENGTH: 257 amino acid
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APPLICANT: Bologn
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10036-2711
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                                                                                                                                                                                                               124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL 183
                                                                                                                             64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
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                                            4 SEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
  4; Gaps
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
APPLICANT: Johan Hansson, Terje Kalland, Lars
APPLICANT: Johan Hansson, Terje Kalland, Lars
APPLICANT: Abrahmsen and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
TITLE OF INVENTION: AND THEIR USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/695,692B
FILING DATE: August 12, 1996
CLASSIFICATION: 530
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Patent No. 6514498
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APPLICATION NUMBER: 9601245-5
FILING DATE: MARCH 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 233 amino acids amino acid
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  Matches 220; Conservative
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Matches 191;
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US-08-695-692B-7
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                                                                                                                                                                                                                                                                  APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dannis M.
APPLICANT: Lambert, Dephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCES: 245
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTG
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                                     205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENWHIDIYLYTS 257
             181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
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82.0%; Pred. No. 1.2e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                          Sequence 113, Application US/08484223B Patent No. 6020459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 787.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                      Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
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NAME: Coruzzi, Laura A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 82.09
Matches 191; Conservative
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STATE: New York
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                      25 SEKSEEINEKDIRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
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82.0%; Pred. No. 1.2e-96;
ive 17; Mismatches 25; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A FILING DATE: CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEB: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
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                                                                                                                                                                                                                               Sequence 123, Application US/08360107A Patent No. 6017536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
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NAME: CORIZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9087
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 82.0
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: · unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                           RESULT 20
US-08-360-107A-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                                                                                                     Sequence 113, Application US/08475668A
Sequence 113, Application US/08475668A
Sequence 113, Application US/08475668A
Sequence 113, Application US/08475668A
Sequence 113, Application US/08475668A
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CCALLZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 3772-026
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas CITY: New York
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; Sequence 113, Application US/08485551A
; Patent No. 6068973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS: LENGTH: 257 amir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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                                                                                                US-08-475-668A-113
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 SEKSEEINEKDLRKKGELQGTALGULKQIYYYNEKAKTENKESHDQFLQHTLLFKGFFTD 84
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205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 06-UIN-1995
ATTORNEY/AGENT INFORMATION:
NAME: 05-UIN-1995
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                    Sequence 113, Application US/08919597
Patent No. 6054265
                                                                                                                                                                                                                                                                      APPLICANT: Barney, Shawn O. APPLICANT: Lambert, Dennis M. APPLICANT: Petteway, Stephen R. APPLICANT: Langlois, Alphonse J
                                                                                                                                                                                             Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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TYPE: amino acid
STRANDEDNESS:
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STATE: New York
COUNTRY: USA
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bologne
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                                                                                                JS-08-919-597-113
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Wild, Carl T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                              APPLICANT: Barney, Shawn O.
APPLICANT: Barney, Shewn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEKSBEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
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                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compartible
COMPUTER: TEM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA A.
REGISTRATION NUMBER: 30, 742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 790-9090
TELEFAK: (212) 869-9741/8864
TELEK: 66141. PENNIE
INFORMATION FOR SEQ ID NO: 113:
                      Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 257 amino acids amino acids
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Best Local Similarity 82.0%
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             New York
: USA
    GENERAL INFORMATION:
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US-08-471-913A-113
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Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: PUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 EEKKVPINLMLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKXNLYNSDVPDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SEKSEBINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHIILFKGFFTD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUITA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAS: (212) 790-9090
TELEPRAS: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.6%; Score 1023; DB 3;
82.0%; Pred. No. 1.2e-96;
tive 17; Mismatches 25;
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Patent No. 6228883
GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 257 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.0
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                  STATE: New York
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FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
VIRUS TRANSMISSION
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                                                                                                                                                                    COUNTRY: USA
ZIP: 1036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILLING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 1023; DB 3;
82.0%; Pred. No. 1.2e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                           STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A. 7.2
REGISTRATION NUMBER: 30, 742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113, Application US/08470896 Patent No. 6479055 GENERAL INFORMATION:
                                           NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 257 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.0% Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-474-349A-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SEKSEEINEKDLRKKKSELQGTALGNLKQ1YYYNEKAKTENKESHDQFLQHTLFKKGFFTD 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING

TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Fanglois, Stephen R.
Fanglois, Stephen R.
VENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.6%; Score 1023; DB 3; Length 257;
82.0%; Pred. No. 1.2e-96;
ive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,264A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 4355
                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CORIZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-99741/8864
  Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 191; Conservative
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APPLICANT: Barney, S
APPLICANT: Lambert,
APPLICANT: Petteway,
APPLICANT: Langlois,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                 CITY: New York
STATE: New York
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                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-485-264A-113
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                      85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNKLT 144
                                                                                                                                                                                                                                                                                                                                                               145 EEKKVPINLMLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                         25 SEKSEBINEKDLRKKSBLQGTALGNLKQIYYYNEKAKTENKESHDQPLQHTILFKGFFTD 84
                                                                                                                                                                                                                                                                                                                      EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKVQ
1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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1155 Avenue of the Americas
                                                                                                                                                                                FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113, Application US/08487266A
Patent No. 6824783
                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECRMUNICATION INFORMATION:
TELEBRHONE: (212) 969-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.0
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New Yor
                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
US-08-487-266A-113
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TITLE OF INVENTION: PUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TANNSMISSION
NUMBER OF SEQUENCES: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 BEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQBKYNLYNSDVFDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SEKSEEINEKOLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTLLFKGFFTD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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82.0%; Pred. No. 1.2e-96;
tive 17; Mismatches 25; Indels
                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/470,896 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Mathews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Marney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                               STATE: New York COUNTRY: USA
                                                                                                                      ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
US-08-485-546A-113
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                                                                                                     COUNTRY:
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Sham O.
APPLICANT: Dambert, Dennis M.
APPLICANT: Detteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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ZIP: 11036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIN PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
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Gaps

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62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
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APPLICANT: Blabile, Robyn E.
APPLICANT: Potter. Terence A.
ITILE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                   Query Match 82.3%; Score 1019; DB 1; Length 233; Best Local Similarity 81.9%; Pred. No. 2.6e-96; Matches 190; Conservative 17; Mismatches 25; Indels (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
CLASSIFICATION 1424
ATYCRNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2879-29-C1
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-9700
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TELEFAX: (303) 863-9700
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1700 Lincoln Street, Suite 3500
                    REGISTRATION NUMBER: 33,005
REFERENCY DOCKET NUMBER: 2879-29
TELEPHONE: (303) 863-023
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
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Patent No. 5935568
GENERAL INFORMATION:
     Kovarik, Joseph E
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MOLECULE TYPE: protein
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TOPOLOGY: linear
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STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                   OFFRANTING SYSTEM: TELLOUS/MD-LOUS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,266A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: COLUZZ, Laura #30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-741/8864
TELEY (212) 869-741/8864
SELEY (212) 869-741/8864
SELEX (212) 869-741/8864
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APPLICATION NUMBER: US/08/446,918A
FILLING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 80203
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelace
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 257 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-487-266A-113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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3 OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS REFERENCE: 09629/005004
                                                         CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-7
EARLIER FILING DATE: 1990-01-7
EARLIER FILING DATE: 1990-01-7
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-7
EARLIER PILING DATE: 1990-01-7
EARLIER PILING DATE: 1990-03
NUMBER OF SEC ID NOS: 34
SOFTWARE: FREESEQ FOR WINDOWS VERSION 3:0
SECTION NO 23
LENGTH: 232
                                             APPLICATION NUMBER: US/09/314,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureas US-09-314-235-23
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                                                                                                                                                                                  EKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                                                                                                                                         2 EKSEEINEKDLRKKSBLORNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTGH
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       GLIVERSEGSTVSYDLFDAQQQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                    ; Score 1019; DB 2; Length 233;
; Pred. No. 2.6e-96;
17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08896933;
Sequence 23, Application US/08896933;
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: FERMAN David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005002;
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER APPLICATION NUMBER: 08/252,978
SANTHARE: RESERVE 1997-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1003.5; DB 3; programmer No. 16-94;
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Patent No. 6338845
GENERAL INFORMATION:
GENERAL TATE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
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                                                                    82.3%;
81.9%;
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Best Local Similarity 81.5%;
Matches 190; Conservative 1.
                                                                      Query Match 82.3%
Best Local Similarity 81.9%
Matches 190; Conservative
      MOLECULE TYPE: protein
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US-09-314-235-23
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US-08-580-806-4
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60 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
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                                                                                                                     1 SEKSBEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                             Gaps
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   DB 3; Length 232;
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US-09-008B-23
Sequence 23, Application US/09708008B
Sequence 23, Application US/09708008B
Secuence 23, Application US/09708008B
Secuence 23, Application US/09708008B
GENERAL INFORMATION:
APPLICANT: FERMAN SUPERANTIGENS, AND RELATED COMPOUNDS;
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REPERBENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-06-02
NUMBER: OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 232
Query Match 81.1%; Score 1003.5; DB 3; Length Best Local Similarity 81.5%; Pred. No. 1e-94; Matches 190; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22 81.1%; Score 1003.5; Best Local Similarity 81.5%; Pred. No. 1e-94 Matches 190; Conservative 16; Mismatches
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SEBE: Charles H. Harris
: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
FORT DETRICK
                                                                              EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                            85 HSWYNDLLVRFDSKDIVDKYKGKKKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
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; Pred. No. 2.7e-94;
17; Mismatches 28
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7:5
SOFTWARE: Microsoft Word 6:0
CURRENT APPLICATION DATA:
FILING DATE: June 25, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/08882431B
; Patent No. 6713284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-7744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
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                                                                                                                                        121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FLING DATE: 01-56p-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/82,431
FILING DATE: «Unknown»
ATTORNEY/AGRYT INFORMATION:
NAME: CHAILSH H. HAIXIS
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-7768-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
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SEQUENCE CHARACTERISTICS:
LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 25
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Matches 188; Conserv
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ADDRESSEE: Charles H. Harris
STREEF: US ARMY MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
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182 GLIVFHTSTERSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233
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80.6%; Pred. No. 6e-94;
                                                                                                                         Sequence 4, Application US/0882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Waccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.3 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION UMBER: US/08/882, FILING DATE: June 25, 1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Charles H. Harris
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.6'
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 40
US-09-350-841A-1599
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                                                                                          RESULT 39
US-08-882-431B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                    205 RGLIVPHTSTEPSVNYDLFGAQGQYSNTLLRIYYBDKTINSENWHIDIYLYTS 257
                                                181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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80.6%; Pred. No. 6e-94;
iive 17; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: CURKNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: CURKNOWN:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPRAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ 1D NO: 4:
US-09-144-776B-4
                                                                                                                                                                                               Sequence 4, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                             APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: FORT DETRICK STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.64
Matches 187; Conservative
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                                                                                                                                                                              US-09-144-776B-4
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121

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67 LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP 126
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS; FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER PILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
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Patent No. 6692746
GENERAL INFORMATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 1907-11-08
FRIOR FILING DATE: 1997-07-18
FRIOR FILING DATE: 1997-07-18
                                                                                                                             182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Indels
                                                                                             187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-09-708-008B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 INLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 SEKSEEINEKDLRKKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTLFKGFFTD 84
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                                                                                GENERAL INFORMATION:
APPLICANT: Jeffs, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: METHODS AND COMPOSITIONS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT PAPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PATENT VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTG
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; Sequence 25, Application US/08896933
; Patent No. 6221351
; APPLICANT: Terman. David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
; FILE REFERENCE: 09629/005002;
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER OF SEQ ID NOS: 34
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FRASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.8%; Score 926.5; DB 4; 79.1%; Pred. No. 8.9e-87; ative 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.1%; Score 657; DB 3; Best Local Similarity 55.6%; Pred. No. 3.2e-59; Matches 125; Conservative 33; Mismatches 67,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599
599, Application US/09350841A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Staphylococcus aureas US-08-896-933-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 79.11
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1599
                                Sequence 1599,
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Length 82;

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', DB 3; L
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100.0%; Pred. No. 2.3
tive 0; Mismatches
                    TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19
                                                                                                                                                                                                                                                                                                   103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08882431B Patent No. 6713284 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                61 KTACMYGGVTLHDNNRLTEEKK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882
FILING DATE: June 25, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 619-2065
TELEPAK: (310) 619-7714
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                Best Local Similarity 100.
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-4318-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-882-431B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                   LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVP 126
                                                                                                                                                                                                                                                                                                                                                                                          62 LLINFNSKEMAQHFKSKNVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNKIKERKKIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 INLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                          2 VEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTDLINFED
                                                                                                                                                                                                                                                                               7 INEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                          Query Match 53.1%; Score 657; DB 4; Length 228; Best Local Similarity 55.6%; Pred. No. 3.2e-59; Matches 125; Conservative 33; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RObert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 0.-Sep-1998
CLASSIFICATION NUMBER: 08/882,431
FILING DATE: -Unknown>
APPLICATION NUMBER: 08/882,431
FILING DATE: -Unknown>
ATTORNEY/ACENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                          NUMBER OF SEQ ID NOS: 34
SOFTHARRE: FASTSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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      PRIOR FILING DATE: 1994-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
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APPLICANT: Robert G. Ulrich,
APPLICANT: Robert G. Ulrich,
APPLICANT: Barvari
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
MUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
ADDRESSE: Charles H. Harris
ATREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                      43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
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Indels
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APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
ADDRESSEE: US ARRY MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STRATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Sequence 2, Application US/08446918A

Patent No. 5705151

GENERAL INFORMATION:

APPLICANT: Elmelie, Robyn B.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 399; DB 4; Length 82;
Pred. No. 2.1e-33;
4; Mismatches 7; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Watch
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882.4
FLING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34.616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.6%;
Matches 71; Conservative
APPLICANT: Mark A. Olson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1700 Linc
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SHDQFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
                                                                                                                                                                                                                           APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: FORM:

COMPUTER: Apple Macintosh
COERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harrish
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: UNKNOWN

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 KTACMYGGVTLHDNNRLTEEKK 124
103 KTACMYGGVTLHDNNRLTEEKK 124
                            61 KTACMYGGVTLHDNNRLTEEKK 82
                                                                                                                                                        Sequence 17, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KTACMYGGVTLHDNNRLTEEKK 82
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; Sequence 17, Application US/08882431B
; Patent No. 6713284
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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RESULT 47

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64 NQEMATLFYDKNVDIYGVEYYHLCYLCENABRSACIYGGVTNHBGNHLBIPKKIVVKVSI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 LGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYIHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 DGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                       1 SEKSEEINEKDLRKKSELORNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 29, Application US/08896933; Patent No. 6221351; Patent No. 6221351; GENERAL INFORMATION: APPLICANT: Terman, David S.; TITLE OF INVENTION: TUMOR KILLING BFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS; FILE REFERENCE: 09629/005002.
; CURRENT APPLICATION NUMBER: US/08/896,933; CURRENT FILING DATE: 1997-07-18; EARLIER APPLICATION NUMBER: 08/252,978; EARLIER FILING DATE: 1994-06-02; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                                       24.2%; Score 300; DB 2; 34.0%; Pred. No. 1.5e-22; tive 46; Mismatches 97
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REFERENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPRAK: (303) 863-023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pyogenes
                                                                                                                                                     : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 35.6%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                           Best Local Similarity 34.0
Matches 83; Conservative
                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 YLYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 LGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 VTLHDNNRLTBEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SMESOPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDOFLYFDLIYSIKDTK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEKSERINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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Patent No. 5935568
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Botter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         24.2%; Score 300; DB 1; Length 255; 34.0%; Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                        PILING DATE: 18-MAY-1995
CLASSIFICATION: 552
PIROBOUC A. CLASSIFICATION: 552
                                                                                           CLASSIFICATION: 552
ATTORNEY/AGENT INPORMATION:
NAME: KOVATIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
                                                                                                                                                                                                                         TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Conservative
                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 YLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 YLTT 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                US-08-446-918A-2
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US-08-580-806-2
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Conservative
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nes 80; Conserva
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Best Local Similarity
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US-08-973-391C-13
                                                                                                                                                            US-09-708-008B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
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                                                                                                                                                                                                                                                               TITLE OF INVENTION: David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS. FILE REFERENCE: 0629/005004

CURRENT APPLICATION NUMBER: 08/09/314,235

CURRENT PILING DATE: 1999-05-18

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1999-06-02

EARLIER FILING DATE: 1992-06-01

EARLIER PILING DATE: 1992-06-01

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-10-03

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PARESQ for Windows Version 3.0
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Fatent No. 6692746
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
FRIOR APPLICATION NUMBER: US/08/896,933
FRIOR FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ESFWFDLFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
                                                                   180 ESFWFDLFPEPEFTOSKY----LMIYKDNETLDSNTSQIEVYLTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 STVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84; Indels
                                            192 STVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.9%; Score 296.5; DB 3;
Best Local Similarity 35.6%; Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Mismatches
                                                                                                                                                                                                  Sequence 29, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
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US-09-708-008B-29
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64 NQEMATLFKDKNVDIXGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scoehr, Jennifer
APPLICANT: Stochr, Jennifer
APPLICANT: Stochr, Jennifer
APPLICANT: Stochr, Jennifer
APPLICANT: Obleades
TITLE OF INVENTION: MURANIS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600.311USWO
CURRENT APPLICATION NUMBER: US/08/973,331C
CURRENT FILING DATE: 1999-03-12
PRIOR PRILING DATE: 1996-06-07
PRIOR PAPLICATION NUMBER: US 08/480,261
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 251
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                                                                                                                                                                                                                                                                           Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 23.8%; Score 294.5; DB 4; Length 2
I Similarity 34.2%; Pred. No. 5.4e-22;
81; Conservative 45; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                    23.9%; Score 296.5; DB 4
35.6%; Pred. No. 2.8e-22;
tive 42; Mismatches 84
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08973391C
Patent No. 682441
GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
                                                                                                                                                TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Streptococcus pyogenes US-08-973-391C-13
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ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SEKSBEINEKDLRKKSELORNALSNLROIYYYNEKAITENKESDDOFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 293.5; DB 4; 32.8%; Pred. No. 7.4e-22; tive 45; Mismatches 100;
                                                                                                                                                                                                          APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                            Sequence 6, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.1 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/882, FILING DATE: June 25, 1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.8%
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: Unkr
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260 YLTT 263
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                                                                                                         US-08-882-431B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AESQPDPKPDELHKSSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
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    ETGYIKFIPKNKESFWFDFFPEPFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.7%; Score 293.5; DB 3; Length 266; Best Local Similarity 32.8%; Pred. No. 7.4e-22; Matches 80; Conservative 45; Mismatches 100; Indels 19;
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                         APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORIEY AGENTE: <UNKNOWN>
ATTORIEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECTIE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         Sequence 6, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                               Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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US-09-708-008B-26
                    LENGTH: 239
SEQ ID NO 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 23.6%; Score 292.5; DB 3; Length 239; I Similarity 34.0%; Pred. No. 8e-22; 82; Conservative 44; Mismatches 96; Indels 19
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FARENT NO. 9.3 1843

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004

CURRENT PILLING DATE: 1999-05-18

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

EARLIER FILING DATE: 1992-06-01

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1990-01-17

EARLIER FILING DATE: 1990-10-03

NUMBER OF SEQ ID NOS: 34

NUMBER OF SEQ ID NOS: 34
                                                                                                                                                 APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REPERENCE: 056229/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER PILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 239
                                                                                   Sequence 26, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
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US-08-896-933-26
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Best Local
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                                                                                                                                                                                                                                                                                                               62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV 111
                                                                                                                                                                                                                                                                                                                                                                                                                   112 TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
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                                                                                                      Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 26, Application US/09708008B
; Batent No. 6692746
; GENERAL INFORMATION:
APPLICANT: Terman. David S.;
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REPRENCE: 09629/005002;
CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR FILING DATE: 1994-06-02
                                                                                                 Query Match 23.6%; Score 292.5; DB 3; Length 2
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 239
TYPE: PRT CREANISM: Staphylococcus aureas US-09-314-235-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus aureas US-09-708-008B-26
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64 NQEMATLFYDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHFGNHLBIPKKIVVKVSI 123
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                                                                                                                                                                                                                                                                                             16 SELQRNAL-SNIRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG
                                                                                                                                                                                                                                                                                                                                                                                  73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWI
                                                                                                                                             DB 4; Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|| ::|| | ::|| | 100 ESFWFDFFPEFFTQSKY----LMIXKDNETLDSNTSQIEVYLTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 STVSYDLFD----AQGOYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                         23.5%; Score 291.5; DB 4
35.1%; Pred. No. 9.1e-22;
tive 42; Mismatches 85
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Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION UNDER:
FILING DATE: -UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: -UNKNOWN>
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09144776B patent No. 6399332 GENERAL INFORMATION:
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (301) 619-2065
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (301) 619-7714
                         ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: FORT DETRICK STATE: MARYLAND
                                                                                                                                                                                                        79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                      Best Local Similarity
Matches 79; Conserv
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LENGTH: 221
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                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mason, Hugh
APPLICANT: Palmer, Kenneth
APPLICANT: Hefferon, Kathleen
APPLICANT: Hefferon, Kathleen
APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
FITLE OF INVENTION: Gene in 1999/414,276
CURRENT APPLICATION NUMBER: US/09/414,276
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.6%; Score 292.5; DB 3; Length 266; 33.2%; Pred. No. 9.4e-22; tive 47; Mismatches 97; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----
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Patent No. 652341
PAPERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
                                                                                                                                                                                                                                        Sequence 8, Application US/09414276 Patent No. 6392121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: bean yellow dwarf virus US-09-414-276-8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 YLYT 232
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                               230 L 230
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US-08-973-391C-14
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ORGANT
                                                                                                                                                                                                                  US-09-414-276-8
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                               82 GPNYDKLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL 141
                                                                                                                                                                          120 TEEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                           81
  4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
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                                                                                                                                                                                                                                                               180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                          198 ETGYIKFIPKONKESFWFDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLIT 250
                           25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: 08/882,431
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REFERENCE/DOCKET NUMBER: 34,616
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
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TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scc
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INFORMATION FOR SEQ ID NO: 10:
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CITY: FORT DETRICK
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23.3%
Best Local Similarity 33.9%
Matches 80; Conservative
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COUNTRY: USA
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ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
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                                                                                                                                                                                                                                                                                                          120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                          25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VS 81
                                                                                                                               4 SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                 180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                          ETGYIKFIPKNKESFWFDFFPBPBFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250
                                                                                        Gaps
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                                           DB 3; Length 251;
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                                                                                      93; Indele
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33.8%; Pred. No. 1.8e-21;
tive 45; Mismatches 93;
                                           23.4%; Score 289.5; DB 3
33.8%; Pred. No. 1.8e-21;
iive 45; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macincon.
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
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Patent No. 6713284
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
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TELEFAX: (301) 619-7714
INFORMATION FOR SEG ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.8%
Matches 80; Conservative
                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Peptide
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STRANDEDNESS: Un
                                      Query Match
Best Local Similarity
Matches 80; Conserv
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US-09-144-776B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEB: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.8%; Score 282.5; DB 3;
32.8%; Pred. No. 1e-20;
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Bacterial Superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PAPPLICATION UNDBER: 08/882,431
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                      Sequence 8, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                               APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Unknown
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CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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nes 80; Conserva
                                                                                                                                                                                     US-09-144-776B-8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 VDLGSKDATNKYKGKKVDLYGAYYGYQCAGG------TPNKTACMYGGVTLHDNNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 LTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                    66 VEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQ 125
                                                                                                        119 LTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHY1.HGKFGLYNSDSFGGK 178
                                                                                                                               7 KPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KKSELQRNA----LSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
                                                                                                                                                                                       179 VQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                            23.3%; Score 288.5; DB 4; Length 239; 33.9%; Pred. No. 2.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bacterial Superantigen TITLE OF INVENTION: Vaccines
                               VDLGSKDATNKYKGKKVDLYGAYYGYQCAGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MICTOSOFT WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 80; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino Acid
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66 ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNG 125
   203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 238;
                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08896933
Sequence 28, Application US/08896933
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/00508/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
SEARLIER PILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 238
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GENERAL INCORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS
FILE REFERENCE: 05629/005004
CURRENT PILLING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER PILLING DATE: 1997-07-18
EARLIER PILLING DATE: 1997-07-18
EARLIER PILLING DATE: 1997-06-01
EARLIER PILLING DATE: 1992-06-01
EARLIER PILLING DATE: 1992-06-01
EARLIER FILLING DATE: 1992-01-17
EARLIER FILLING DATE: 1992-01-17
EARLIER FILLING DATE: 1990-01-17
NUMBER: OF SEQ ID NOS: 34
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                                                                        229 YLYT 232
                                                                                                                                         260 YLTT 263
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-09-314-235-28
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STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                           203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKMYDSKDVKIEV 259
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171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
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22.8%; Score 282.5; DB 4; Length 266;
Best Local Similarity 32.8%; Pred. No. 1e-20;
Matches 80; Conservative 46; Mismatches 99; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert G. Ulrich,
APPLICANT: Rak A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882.45
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 266

LENGTH: 266

***AMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
***LENGTH: 266
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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                                                                                                                                                                                                      260 YLTT 263
                                                                                                                                         229 YLYT 232
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US-08-896-933-27
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                                                                                                                                                                                                                                                                                                        66 ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNG 125
                                                                                                                                                                                                                                                                                                                                                           123 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                 11 DLRKKSELQRNALSNIRQIYYYNEKAITENK-ESDDQFLENTLIFKGFFTGHPWYNDLLV
                                                                                                                                                                                                        11 DLRKKSBLQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RGLIVFHSSEGSTVSYDLFDAOGOYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                               22.7%; Score 281.5; DB 3; Length 238; 32.5%; Pred. No. 1.1e-20; tive 47; Mismatches 92; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.7%; Score 281.5; DB 4; Length 238; ilarity 32.5%; Pred. No. 1.1e-20; Conservative 47; Mismatches 92; Indels 19
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APPLICANT: Terman. David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT PAPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR PILING DATE: 1997-07-18
PRIOR PILING DATE: 1997-07-18
PRIOR PILING DATE: 1997-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
 SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6692746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureas US-09-708-008B-28
                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-28
                                                                                                                                                                      76; Conservative
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Best Local Similarity
                                                                                                                                                     Local Similarity
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LENGTH: 238
                       SEQ ID NO 28
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                                                                                                                                   Query Match
                                 LENGTH:
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RESULT

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62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLH 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 DSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYL
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CHERALI INFORMATION:
CHERALI INFORMATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER FILING DATE: 1997-07-18
EARLIER PILING DATE: 1997-07-18
EARLIER FILING DATE: 1992-06-01
EARLIER FILING DATE: 1992-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
SEARLIER FILING DATE: 1990-01-17
SEARLIER PRILING DATE: 1990-01-17
SEARLIER FILING DATE: 1990-01-17
SEARLIER PRILING DATE: 1990-01-17
SEARLIER PRILING DATE: 1990-01-17
SOFFWARE: FREESED FOR WINDOWS 34
Sequence 27, Application US/08896933
Sequence 27, Application US/08896933
GENERAL INCORPATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER PILLING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOOFWARRE: FastsEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 239
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31.0%; Pred. No. 2.9e-19;
iive 49; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.03
Matches 75; Conservative
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SEQ ID NO 27
LENGTH: 239
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111 VTLHDNNRLTE-EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHID 227
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GENERAL INFOGRATION:
GENERAL INFOGRATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-06-02
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17

EARLIER FILING DATE: 1990-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
21.0%; Score 260.5; DB 3; Length ;
Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 78; Conservative 47; Mismatches 97; Indels
                                                                                                                                                                               APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASHSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
                                                                                                                ; Sequence 21, Application US/08896933; Patent No. 6221351; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-21
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VYLTT 236
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  235 TT 236
                                                                                          US-08-896-933-21
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                                                                                                                                                                                                                                                                                                                                                                                         59 KNYDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKH 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLH 114
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                                                                                                                     17; Gaps
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                                                                        Length 239;
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pactent No. 6692746

GENERAL INFORMATION:
TITLE OF INVENTION:
SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/00502
CURRENT APPLICATION NUMBER: US/08/896,933
PRIOR APPLICATION NUMBER: US/08/896,933
PRIOR APPLICATION NUMBER: 08/252,978
PRIOR PILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
LENTH: 239
                                                                                                                     Indels
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                                                                      Query Match 21.6%; Score 267.5; DB 3; Best Local Similarity 31.0%; Pred. No. 2.9e-19; Matches 75; Conservative 49; Mismatches 101;
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  ; ORGANISM: Staphylococcus aureas US-09-314-235-27
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Gaps

23;

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172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
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175 YERNN--SPYETGYIKFIENENS-FWYDMMPAPGNKFDQSKYLMMYNNDKMVDSKDVKIE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.9%; Score 258.5; DB 3;
30.0%; Pred. No. 2.9e-18;
tive 51; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Bacterial Superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDMESS: Unknown
TOPOLOGY: Unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-7768-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                            US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 639933.2
; GENERAL INFORMATION:
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TELEPHONE: (301) 619-2065
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Mark A. Olson
Sina Bavari
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Atty)
CITY: FORT DETRICK
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Matches 73; Conserv
                                                                                                                             236
                                                                      228 LYLYT 232
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232 VYLT
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                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTLHDNNRLTE-EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHID 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTLHDNNRLTE-EKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 VTEHGNNQLDKYYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVRNKKL 174
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                                                                                                                                                                                                                          DB 3; Length 239;
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; Patent No. 6692746
; GENERAL INFORMATION:
    APPLICANT: Terman. David S.
    TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
    TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002;
    CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR FILING DATE: 1994-06-02
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Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 78; Conservative 47; Mismatches 97; Indels
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31.8%; Pred. No. 1.5e-18;
iive 47; Mismatches 97
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 239
                  SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-314-235-21
                                                                                                                                                                                                                                                                                    78; Conservative
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Best Local Similarity
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                                                    SEQ ID NO 21
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71 LGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYN---VSGPNYDKLKTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 SEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                      Sequence 20, Application US/08896933
Fatent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
BARLIER APPLICATION NUMBER: 08/252,978
BARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FABRES FABRES FOR Windows Version 3.0
SEQ ID NO 20
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APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION UNMERS: 08/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER PILING DATE: 1997-07-18
EARLIER PILING DATE: 1997-07-18
EARLIER FILING DATE: 1997-00-1
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1992-06-01
EARLIER FILING DATE: 1992-06-01
EARLIER FILING DATE: 1991-00-01
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
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19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Streptococcus pyogenes
                             230 LYT 232
                                                                            261 LTT 263
                                                                                                                                                                              US-08-896-933-20
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STREET: US ARMY MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 FNS--SFYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
203 FNS--SFYETGYIKFIENNGNIFWYDMMPAPGDKFDQSKYLMMYNDNKIVDSKSVKIEVH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.9%; Score 258.5; DB 4; Best Local Similarity 30.0%; Pred. No. 2.9e-18; Matches 73; Conservative 51; Mismatches 102;
                                                                                                                                                                                                                                             Sequence 14, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
TITLE OF INVENTION: Wactines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/882,431B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPERATING SYSTEM: MACINICOBI
OPERATING SYSTEM: MACINICOBI
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,43
FILING DATE: June 25, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INPORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 619-7014
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino Acid
                                                                            230 LYT 232
                                                                                                                              261 LTT 263
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RESULT 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 WIDGKQT-TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 LGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINL 129
                                                                                                                                                                                                                                                                                                          62 LKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKV 121
                                                                                                                                                                                                                                                                                                                                                                 130 WIDGKOT-TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHS 188
                                                                                                                                                                                                                                                                                                                                                                                           14 KKSELQRNALSNLRQIYYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
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                                                                                                                                                                                                14 KKSELORNALSNIRQIYYYNEKA--IT-ENKESDDOFLENTLLFKGFFTGHPWYNDLLVD
                                                                                                                                                                                                                                           5 KPSQLQRSNLVKTFKIYIPFMRVTLVTHENVKSVDQLLSHDLIYN----VSGPNYDKLKTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 SEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 245; DB 4; Length 220;
30.7%; Pred. No. 5.3e-17;
tive 42; Mismatches 94; Indels
                                                                                                                  Query Match
19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/708,008B CURRENT FILING DATE: 2000-11-08 PRIOR PILING DATE: 1997-07-18 PRIOR PLING DATE: 1997-07-18 PRIOR PLING DATE: 1994-06-02 SOFTWARE: FASTSO FOR WINDOWN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09708008B
Patent No. 6692746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Streptococcus pyogenes
                                        ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20
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Best Local Similarity 30.71
Matches 70; Conservative
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LENGTH: 220
                       LENGTH: 220
SEQ ID NO 20
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RESULT 81 US-09-144-776B-18

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45 DQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKT 104
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                                                                                                                                                                                                                                                               ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
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; Sequence IN. 6713284
; Patent No. 6713284
; GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
ITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
Sequence 18, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                     CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Mord 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-56p-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 08/82,431
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/82,431
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/82,431
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 04 HATTIS
REFERENCE/DOCKET NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: UNKNOWN; MOLECULE TYPE: Peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-144-776E-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 ACMYGGVTLHDNNRLTEEKK 124
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STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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Gaps
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Fatent No. 3859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
15.4%; Score 191; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.8e-12;
Matches 39; Conservative 1; Mismatches 5; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 12-AUG-1996

CLASSIFICATION NUMBER: 08/08/696,012

FILING DATE: 29-MAR-1996

FILING DATE: 29-MAR-1994

APPLICATION NUMBER: 08/220,378

FILING DATE: 29-MAR-1994

APPLICATION NUMBER: US 07/941,497

FILING DATE: 530

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 11,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
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NAME: Saliwanchik, David R.
REGISTATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-220-378-1
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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STATE: FL
COUNTRY: US.
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-696-012-1
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    : US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
FORT DETRICK
MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 DQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DQFLENTLLYKKFFTDLINFEDLLINFNSKEMAQHFKSKNVDVYPIRYSINCYGGEIDRT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
                                                                                             ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 ACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/POCKET NUMBER:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                               COUNTRY:
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84 ------KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLMIDGK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDS--PGGKVQRGLIVFHSSEGS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 NH--KLLGNLFISGESQQNLNNKIILEKDIVIFQEIDFKIRKYLMDNYKIYDATSPYVSG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 YKGK-------KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 YRGKDYYISSEMSYEASQKFKRDDHVDVFGLFYILNSHTG-----EYIYGGITPAQNNKV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PW-YNDLLVDLGSKDA----TNK 79
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                                                                                                                                                                                                                                                                                                                                                           Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 30, Application US/08896933; Patent No. 6221351; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.; TITLE OF INVENTION: TURER KILLING EPFECTS OF ENTEROTOXINS; TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS; TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS; CURRENT APPLICATION NUMBER: US/08/896,933; CURRENT FILING DATE: 1997-07-18; EARLIER FILING DATE: 1997-07-18; EARLIER FILING DATE: 1994-06-02; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; ELENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 NKESDDOFLENTLLFKGFFTGHPW-YNDLLVDLGSKDA----TNKYKGK
                                                                                                                                                                                                                                                                                                                                                             14.8%; Score 183.5; DB 4; Length; 25.8%; Pred. No. 1.2e-10; tive 37; Mismatches 73; Indels
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FILE REFERENCE: 600.347USWO
CURRENT APPLICATION NUMBER: US/09/308,829
CURRENT FILING DATE: 1999-07-14
PRIOR PILING DATE: 1997-12-05
PRIOR FILING DATE: 1997-12-06
PRIOR PILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptococcus pyogenes US-09-308-829-2
                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local
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APPLICANT: Schlievert, David T.
APPLICANT: Oblendorf, Douglas
APPLICANT: Oblendorf, Douglas
APPLICANT: Mitchell, David T.
APPLICANT: Mitchell, David T.
APPLICANT: Mitchell, David T.
APPLICANT: Gahr, Pamala M.
TITLE OF INTENTION: MITANTION: OF STREPTOCOCCAL TOXIN C AND-METHODS OF USE
TITLE OF INTENTION: MITANTION: 1999-06-18
FILE REFERENCE: 600.347USI1
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 60/091,864
PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-05
PRIOR PELING DATE: 1997-12-05
PRIOR PELING DATE: 1996-12-06
PRIOR PELING DATE: 1996-12-06
PRIOR PELING DATE: 1996-12-06
SHORD FILING DATE: 1996-12-06
SHORD FILING DATE: 1996-12-06
SHOWBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
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Patent No. 6835818
GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Ohlendorf, Douglas
APPLICANT: Mitchell, David T.
APPLICANT: Gahr, Pamala J.
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 KVQRGLIVPHSSEGSTVSYDLFDA--QGQYPDTLLRIYRDNKTINSENL-HIDLYL 230
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                                                                                                        Length 45
                                                                                                                                                                                                                            1 SEKSEEINEKULRKKSELQGTALGNLKQIYYYNEKAKTENKESHD 45
                                                                                                                                                    5; Indels
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                                                                                                   15.4%; Score 191; DB 2; 86.7%; Pred. No. 1.8e-12; ative 1; Mismatches 5;
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Patent No. 6774218
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; ORGANISM: Streptococcus pyogenes
US-09-336-036-2
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                                                                                                        Query Match
Best Local Similarity 86.77
Matches 39; Conservative
                                MOLECULE TYPE: peptide
            linear
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Best Local Similarity
Matches 61; Conserv
            TOPOLOGY:
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US-09-308-829-2
                                     , MOLECULE T)
US-08-696-012-1
                                                                                                                                                                                                                                                                                                                                              US-09-336-036-2
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDS--FGGKVQRGLIVFHSSEGS 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FERENT NO. 03 38 8440:

FORENEAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

TITLE OF INVENTION: UPPERANTIGENS, AND RELATED COMPOUNDS

FILE REFERENCE: 09629/005004

CURRENT FILING DATE: 1993-05-18

EARLIER FILING DATE: 1993-05-18

EARLIER FILING DATE: 1993-06-01

EARLIER FILING DATE: 1994-06-02

EARLIER FILING DATE: 1994-06-01

EARLIER FILING DATE: 1992-06-01

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1990-01-17

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TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE OF INVENTION SUPERANTIGENS, AND RELATED COMPOUNDS FILE OF SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO SOLOSO S
193 TVSYDLFDA--QGQYPDTLLRIYRDNKTINSENL-HIDLYL 230
                                                          167 HEQIDLFDSPNEGTRSDIFAK-YKDNRIINMKNFSHFDIYL 206
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27.1%; Pred. No. 1.6e-10;
tive 41; Mismatches 75;
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                                                                                                                                                                                                                                                                                                      5-09-314-235-30
Sequence 30, Application US/09314235
Patent No. 6338845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus pyogenes
US-09-314-235-30
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Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 ------KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDS--FGGKVQRGLIVFHSSEGS 192
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                                                                                                                                                                                                                                                                                                                                                                                                                   45;
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                                                                                                                                                                                                                                                                                                          14.7%; Score 181.5; DB 4; Length 208; 27.1%; Pred. No. 1.6e-10; tive 41; Mismatches 75; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 TVSYDLFDA--OGOYPDTLLRIYRDNKTINSENL-HIDLYL 230
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ADDRESSEB: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
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Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
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APPLICATION NUMBER: 08/882,431
FILING DATE: «Unknown»
ATTORNEY,AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: «Unknown»
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CLASSIFICATION: <Unknown>
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TELEPHONE: (301) 619-2065
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(301) 619-7714
SEQ ID NO 30
LENGTH: 208
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-708-008B-30
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STRANDEDNESS: Unknown
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SEQUENCE CHARACTERISTICS
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CITY: FORT DETRICK
STATE: MARYLAND
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Best Local Similarity 27.1'
Matches 60; Conservative
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60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86

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Gaps
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APPLICANT: Johnson, Howard M.
APPLICANT: Johnson, Howard M.
APPLICANT: Pentzer, Carol H.
APPLICANT: Brontzer, Carol H.
APPLICANT: Strain Strain Strain Street, Sulte Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Sulte A-1
                                                                                                                                                       APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
                                                                                                                                                                                                                                                                                            SSEE: Saliwanchik & Saliwanchik
1: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 ENKESDDQFLENTLLFKGFFTGHPWYND 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08696012
Patent No. 5859207
                                                                   US-08-220-378-2; Sequence 2, Application US/08220378; Patent No. 5545716
GENERAL INFORMATION: APPLICANT: Johnson, Howard M.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
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Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 32606
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US-08-696-012-2
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STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
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                                                                                                                            Indels 11;
                                                                                                                                                                         43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC
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11.1%; Score 137.5; DB 4; Length 89;
Best Local Similarity 39.1%; Pred. No. 1.5e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 1.
                                                                                     Length 89;
                                                                                 Query Match 11.1%; Score 137.5; DB 3; Best Local Similarity 39.1%; Pred. No. 1.5e-06; Matches 34; Conservative 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 ----AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                            97 ---- AGGTPNKTACMYGGVTLHDNNRL 119
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20
                                                                                                                                                                                                                                                                                       60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFRAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June 25, 1997
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Unknown
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MOLECULE TYPE: Peptide
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CORRESPONDENCE ADDRESS:
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US-08-882-431B-20
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US-08-220-378-5

Sequence 5, Application US/08220378

Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. No. Patent No. No. Patent No. No. Patent No. Patent No. No. Patent No. No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Pat
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MEDIUM TYEE: PLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.3%; Score 127; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 24; Conservative 0; Mismatches 0;
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CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPERBNCE/DOCKET NUMBER: 31,794
TELECHONE: 904-375-8100
TELEFRX: 944-375-8100
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                                        NAME: MORRY, WARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-
TELECOMMUNICATION INPORMATION:
TELEPAN: (212)758-6849

INPORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
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Best Local Similarity
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COUNTRY: US
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-838-413A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-220-378-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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           COUNTRY: LEST COUNTRY: LOSA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION NUMBER: US 09/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 28-MAR-1992
CLASSIFICATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
TELEFOMMUTICATION INFORMATION:
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TELEFOMMUTICATION INFORMATION:
TELEFOMMUTICATION INFORMATION:
TELEFOMMUTICATION INFORMATICS:
LENGTH: 28 amino acids
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; Sequence 22, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
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; MOLECULE TYPE: peptide
US-08-696-012-2
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CLASSIFICATION: 536
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 94
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DB 1; Length 29;
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APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
  Superantigen Agonist and Antagonist Peptides
                                                                                                                                                                                                  COMPTIER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 124; DB 1;
Pred. No. 7e-06;
4; Mismatches
TITLE OF INVENTION: Superantigen Agonist ar TITLE OF INVENTION: Peptides
OWNERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Ablwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 EEKKVPINLWIDGKQTTVPIDKVKTSKK 148
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08 6.SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELEPHONE: 904-375-8100
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12-AUG-1996
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Patent No. 5859207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.0.
These 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gainesville
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                                                                                                                            CITY: Gai
STATE: FI
COUNTRY:
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        Gaps
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APPLICANT: Pontzer, Carol H.
APPLICANT: Origgs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
      0; Indels
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSITICATION DATA:
APPLICATION NUMBER: US/09/696,012
FILING DATE: 29-AMR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: SO
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 17,794
REFERENCE/DOCKET NUMBER: 17,794
REFERENCE/DOCKET NUMBER: 17,794
REFERENCE/DOCKET NUMBER: 17,794
REFERENCE/DOCKET NUMBER: 17,794
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                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%; Score 126; DB
100.0%; Pred. No. 3.1
tive 0; Mismatches
        0; Mismatches
                                                102 NKTACMYGGVTLHDNNRLTEEKK 124
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Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Griggs, Nathan D.
                                                                                                                                                                     US-08-696-012-5; Sequence 5, Application US/08696012; Patent No. 5859207; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
        23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:

// TOPOLOGY: linear
// MOLECULE TYPE: peptide
US-08-696-012-5

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STRANDEDNESS: si
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          Matches
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ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                           43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTP 101
                                                                                                                                                                                                                                                                                                         9.8%; Score 121; DB 3; Length 79; 34.6%; Pred. No. 6.1e-05; tive 15; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
TITLE OF INVENTION: Vaccines
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                    TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08882431B Patent No. 6713284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEPAK: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      102 NKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             S8 ERSACIYGGVTNHEGNHL 75
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OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                               27; Conservative
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TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                       Query Match
Best Local Similarity
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ADDRESSEE: Charles H. Harrie
STREET: US ARMY MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION:
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDLUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRIT APPLICATION DATA:
FILLING DATE: 01-589-1998
CLASSIFICATION: <u cliptum company
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NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/POCKET NUMBER: - Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 124; DB 78.6%; Pred. No. 7e-Cative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EEKKVPINLWIDGKQTTVPIDKVKTSKK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEKKVPINLWLDGKQNTVPLETVKTNKK 28
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APPLICATION NUMBER: 08/882,431
FILING DATE: <UNKNOWN>
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDRAR:
APPLICATION UNDRAR: 08/220,378
FILING DATE: 29-WAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP126.C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ.10 NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                      29 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-696-012-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Best Local Similarity
Matches 22; Conserv
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102 NKTACMYGGVTLHDNNRL 119 ::||:||||| | : | 58 ERSACIYGGVTNHEGNHL 75

Search completed: July 26, 2005, 11:09:10 Job time: 28 secs

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Aar45011 Staphyloc Abu79068 S. aureus Adf43288 Staphyloc Abb76234 Staphyloc	Abb79501 Staphyloc Abu10081 Staphyloc Abu62248 S. aureus Aae37676 Protein # Aay54463 Amino aci Abb79502 Staphyloc		Abul0098 Staphyloc Aby70102 Staphyloc Aay70102 Mutant Et	Adfivor	Adf43294 Staphyloc Adf89829 Staphyloc	Aar45013 Staphyloc Aar45013 Staphyloc Abh76236 Staphyloc	Adrillos Staphyloc Adrillos Staphyloc Abm70958 Staphyloc	Abu10091 Bacterial Abu62338 S. aureus	Abul0089 Bacterial Abu62336 S. aureus Aaw24299 Staphyloc	ADDS8460 STADNYIOC Adf89833 Staphyloc Adf89834 Staphyloc	Adf89837 Staphyloc Abp29357 Streptoco Adf89838 Staphyloc	Adf89832 Staphyloc Adf89836 Staphyloc Abu79069 S. aureus	Abg75015 S aureus Adf43290 Staphyloc Aaw06737 Staphyloc	Adf89825 Staphyloc Aaw64647 Synthetic	Aab67341 Staphyloc Abg75016 Unidentif	Ad114247 Wild type Aaw12153 Streptoco	Abu62455 S. aureus Aar13209 Streptoco	Aar45017 Staphyloc Abh76240 Staphyloc	Aaw12151 Streptoco	Aawl2150 Streptoco Adf89839 Streptoco	Aaw12154 Streptoco	Aawi2146 Streptoco Aawi2097 Streptoco	Aawl2147 Streptoco				93		Aab67344 Streptoco Aar13206 Staphyloc	014
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1013 81. 1013 81. 1013 81.	30 1000 80.8 31 1000 80.8 32 1000 80.8 34 996 80.5 35 996 80.5	996 80.	987 79.	830	663 53.	657 53.	649 52. 523 42.	457 36. 457 36.	399 399 370	366 29. 366 29. 339.5 27.	337 27. 336.5 27. 320 25.	319.5 25. 310 25.	300.5 24.	299.5 24. 299.5 24.	299.5 24. 299.5 24.	299.5 24. 297.5 24.	297.5 24. 296.5 23.	296.5 23.	296.5 23.	295.5 23.	294.5 23.	294.5 23.	294.5 23.	294.5 23. 294.5 23.	293.5 23.	293.5 23. 293.5 23.	293.5	293.5 *	292.5	292.5
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5.1.6 Compugen Ltd.	ime 72 Seconds 1t alignments) 00 Million cell updates/sec	RDNKTINSENLHIDLYLYTT 233			: 2105692							predicted by chance to have a score of the result being printed,		Description	Abp58456 Staphyloc	03 68	Adf89830 Staphyloc Aab67339 Staphyloc		5.0	Abu79072 S. aureus	יא פ	Abb76235 Staphyloc Aar13204 Staphyloc	S	Abp58454 Engineere Aar13203 Staphyloc	0.00	Aau14104 Peptide s Abo10269 S. aureus	9 9	Adh10956 Enterotox Aaw06738 Staphyloc	Adi95318 OSPF-rela Aaw35373 Staphyloc	38
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compu	protein search, using sw model July 26, 2005, 10:57:03 ; Search time (without al	US-09-900-766-7 1238 1 SEKSEEINEKDLRKKSELQRRD	BLOSUM62 Gapop 10.0 , Gapext 0.5	2105692 seqs, 386760381 residues	of hits satisfying chosen parameters:	seq.length: 0 seq.length: 200000000	Match Match	′ے ت	1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:*			No. is the number of results predicted greater than or equal to the score of derived by analysis of the rotal scor	SUMMARIES	Query core Match Length DB ID	100.0 233 6	100.0 257 4 100.0 257 6	100.0 257 8 98.9 230 4	98.7 245 2	97.1 245 2	96.0 248 6	95.2 230 2	94.9 230 5	89.4 233 6	89.4 672 6 83.6 233 2	82.6 233 6	82.6 257 4 82.6 257 6	82.6 257 7	82.6 257 8 82.3 233 2	1019 82.3 233 8 ADI95318 1016 82.1 233 2 AAW35373	82.1 233 4

250 20.2 209 8 ADG69998 Adg69998 Adg69998 247.5 20.0 209 8 ADG70011 Adg69999 247.5 20.0 209 8 ADG70011 Adg69999 247.5 20.0 209 8 ADG70010 Adg69999 247.5 20.0 209 8 ADG70010 Adg6999 245.5 19.8 250 6 ABU79074 Add79074 245 19.8 250 7 ADF89845 Adg69845 Adg69845 230 19.3 209 8 ADF89845 Adg69845 Adg69845 20.5 17.8 248 3 AAY93742 Adg699826 Adg699826 220.5 17.8 234 3 AAY93742 Adg69992 Adg69992 Adg69992 Adg69992	Adřebs43 Abulo090 Abulco33743 Abg29358 Abg29358 Adře3928 Adře3928 Adře3928 Adře3928 Adře3928 Adře3928 Adře3928 Adře3928 Adře3928 Adře2788 Adře2788 Adře2788 Adře2788 Adře2788 Adře2788 Adře2788 Adře2788 Adře2788	RESULT 1 ABP58456 ID ABP58456 standard; protein; 233 AA. XX AC ABP58456, XX DT 14-APR-2003 (first entry) XX DE Staphylococcal enterotoxin E.	KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour; KW Cytostatic; vaccine. KW XX XX OS Staphylococcus sp. KX XX PD 09-JAN-2003. XX PF 19-JUN-2002; 2002WO-SE001188. XX PF XX	g G, Erlandssor 13-201467/19. Te for therapy, and four regit patibility compres. Te and four regit patibility compres. Te and four regit set sequence is oxin SEE. The ir
Aay92319 Plant-opt Abu62453 S. aureus Abb76237 Staphyloc Abu62460 Streptoco Aaw59798 Amino aci Aaw5798 Amino aci Aay70109 Streptoco Abb19508 Streptoco Abu62331 Streptoco Abu62331 Streptoco Aay54464 Amino aci	Aay06253 Staphyloc Abb10085 Staphyloc Abu10085 Staphyloc Abu62328 S. aureus Aa97680 Protein # Aay54465 Mutant St Aay70166 Mutant St Aay7016 Mutant St Aay7016 Mutant St Abg71372 Staphyloc Abg71372 Staphyloc Abg71372 Staphyloc Abg71372 Staphyloc Abg71371 Staphyloc Ad114256 Modified Abg71371 Staphyloc Ad114256 Streptoco Aww12149 Streptoco Aww12152 Streptoco Aww12152 Streptoco		Adge Subs Amano aca Aar12208 Staphyloc Aay06258 Staphyloc Abg71373 Staphyloc Abg71374 Staphyloc Abg71374 Staphyloc Aar12207 Staphyloc Aar12207 Staphyloc Abf838 Staphyloc Abf89842 Streptoco Abu79070 S. aureus Adf81292 Staphyloc Aay06251 Staphyloc Aab67342 Staphyloc Aab67342 Staphyloc	. w w w w w w w w w w w w w w w w w w
292.5 23.6 266 3 291.5 23.5 23.6 7 290.5 23.5 23.7 289 289.5 23.4 251 2 289.5 23.4 251 2 289.5 23.4 251 2 289.5 23.4 251 2 289.5 23.4 251 5 289.5 23.4 251 6 289.5 23.4 251 6 289.5 23.4 251 6	1 288.5 23.3 239 2 AAY06253 288.5 23.3 239 5 ABB79505 288.5 23.3 239 5 ABB79505 288.5 23.3 239 7 ABB79505 288.5 23.3 239 7 ABB79505 288.5 23.3 240 6 ABG71369 287.5 23.2 240 6 ABG71370 287.5 23.2 240 6 ABG71372 287.5 23.2 240 6 ABG71372 285.5 23.1 239 8 AAY70255 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.1 240 6 ABG71371 285.5 23.0 251 2 AAW12149 284.5 23.0 251 2 AAW12149 284.5 23.0 251 2 AAW12149	284.5 23.0 266 7 283.5 22.9 240 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	276.5 22.3 228 4 276.5 22.3 239 2 276.5 22.3 239 2 276.5 22.3 240 6 276.5 22.3 240 6 276.5 22.3 240 6 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 267.5 21.6 239 2 265.5 21.5 266 8 265.5 21.5 266 7 265.5 21.4 239 4	265.5 258.5 258.5 258.5 258.5 258.5 258.5 20.9 266.5 258.5 20.9 266.7 256.5 20.9 266.7

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SEE, and an antibody molety, such as tumour reactive antibody 574. The superantigen is engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The conjugates are designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
                                                                                                                                                                                                                                                                                  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
                                                                                                                                                                                                                                                                                                                                                                         1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                     121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                 Gaps
superantigen, such as novel SEA/E-120 (see ABP58455), which is based
                                                                                                                                                                                                                                                                                                                                                                                                                       RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                Length 233;
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                                                                                                                                                                                   Indels
                                                                                                                                              100.0%; Score 1238; DB 6;
100.0%; Pred. No. 7e-116;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 41; 259pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU14103 standard; peptide; 257
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                                                                                                                                                                                 Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442157/47
                                                                                                                                                                   Similarity
                                                                                                                Sequence 233 AA;
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Best Local (
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formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents a peptide sequence from Staphylococcus aureus enterotoxin type
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effective
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                                                                                                                                                                                                                                                                                                                                                                                                                                  145 EEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                                                                                                                                                                                                            85 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                              EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                                                                                                                                              25 SEKSBEINEKDLRKKSELORNALSNIRQIYYYNEKAITENKESDDOFLENTLLPKGFFTG
                                                                                                                                                                                                                                                                                                                                              61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                 1 SEKSEEINEKDLRKKSELORNALSNLROIYYYNEKAITENKESDDOFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting transmission of Epstein-Barr virus to a cell, by contactir
the cell with a peptide consisting of a region of Epstein-Barr virus
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV; Epstein-Barr virus infection; heptad repeat motif.
                                                                                                                                                                                                                   Length 257;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to inhibiting (M) transmission of virus to a cell, comprising contacting the cell with an
                                                                                                                                                                                                               100.0%; Score 1238; DB 4;
100.0%; Pred. No. 8.1e-116;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO10268 standard; protein; 257
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94US-00255208.
94US-00360107.
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                                                                                                                                                                                                                                  Local Similarity 100.
nes 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. aureus enterotoxin E.
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                                                                                                                                                                                    Sequence 257 AA;
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concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTE, 107x178x4 or PLZIP sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group, or macromolecular carrier group, and Z comprises a carboxyl group, amido group, hydrophobic group, or macromolecular carrier group, and clustical of the virus to the call is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motific containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a protein from a pathogenic organism analysed for regions analogus to DP107 or DP178
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                                                                                                                                                                                                                                                                                                                                                                                  121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                                                                                                                                                                                                                                  SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 84
                                                                                                                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superantigen; SAg; Staphylococcal enterotoxin; SE; SEE; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1238; DB 6; Length 257;
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                              ; Pred. No. 8.1e-116; 0; Mismatches 0;
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2002US-0406697P.
2002US-0406750P.
2002US-0415310P.
2002US-0415400P.
2003US-0438686P.
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                                                                                                                                                                                                                                                                                 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus sp.
                                                                                                                                                                                                                                              Sequence 257 AA;
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28-AUG-2002;
29-AUG-2002;
01-OCT-2002;
02-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy;
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                                                                                                                                                                                                                                                                     Query Match
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin B (SEB) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                           Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEKSEEINEKDLRKKSELORNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1238; DB 8; Length 257; 100.0%; Pred. No. 8.1e-116; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus enterotoxin E protein.
                                                                                                                                                                                        Disclosure; SEQ ID NO 7; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour; cancer; immune; enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67339 standard; peptide; 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00416530.
90US-00466577.
91WG-US000342.
92US-00891718.
93US-00189424.
95US-00491746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
WPI; 2004-011997/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 257 AA;
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02-MAR-1993;
31-JAN-1994;
19-JUN-1995;
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antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an
                                                                                                      Tumor cell capable of stimulating antitumor immune reactivity in vitro or
in vivo comprises exogenous nucleic acids encoding a superantigen and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment; cancer; infection; autoimmune disease; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEBINEKOLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                   SEEINEKOLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                                                                                                                                                                                                  present invention relates to a tumour cell capable of stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "can be mutated at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "can be mutated at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "can be mutated at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "can be mutated at this position'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus enterotoxin SEE wild-type superantigen
                                                                                                                                                                                                                                                                                                                                                     98.9%; Score 1224; DB 4; L 100.0%; Pred. No. 1.8e-114; Ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           anticancer immune response in vivo or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35374 standard; peptide; 245 AA
                                                                                                                                                                    Disclosure, Fig 2; 16pp; English
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                                                                                                                                                                                                                                                                                                                                                                                      Matches 230; Conservative
                                                                                                                                        costimulatory molecule.
                                                                        WPI; 2001-158657/16
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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              (TERM/) TERMAN D
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                                                                                                                                                                                                                                                                                                                           Sequence 230 AA;
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                                             Terman DS
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Length 230; 0; Indels

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This is the wild-type Staphylococcus enterotoxin SEB superantigen. This SEB superantigen can be modified to be used in a novel conjugate. The novel conjugate comprises a target seeking moiety and a modified wild type superantigen. The modified superantigen retains its ability to activate a subset of T cells, even though 1 or more wild-type amino acid cativate a subset of T cells, even though 1 or more wild-type amino acid cativate in at least 1 region which functions in determining binding to T cell receptor (TCR) and activation of a subset of T cells has/have been corpugate with a target seeking moiety, for activating the immune or system to treat a mammanian disease. A pharmaceutical composition can be prepared comprising a modified antibody (preferably a Fab fragment tused to a peptide moiety providing activation of T cells in Vbeta specific to a peptide moiety providing activation of T cells in Vbeta specific to a peptide moiety providing activation of T cells in Vbeta specific to prohibit cysteine formation. The modified wild-type superantigen is used conting and in the modified wild type superantigen has a lower immunogenicity and reactivity with neutralising antibodies and has fewer immunogenicity and reactivity with neutralising antibodies and has fewer immunogenicity and reactivity with neutralising antibodies and side-effects when used as a drug, compared to wild type superantigen
                                                                                                                                                                                                                                        Conjugate of target seeking moiety and modified superantigen - useful for activating the immune system to treat cancer, viral infections, parasitic infestations and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RGLIVPHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNK-----TINSENLHIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.7%; Score 1222; DB 2; Length 245; Best Local Similarity 95.1%; Pred. No. 3.1e-114; Matches 233; Conservative 0; Mismatches 0; Indels 1.
                                                                                                                                         Kalland
                                                                                                                                         Bjoerk P, Dohlsten M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP58457 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                            Claim 4; Page 38-39; 58pp; English.
                                                                                                   (PHAA ) PHARMACIA & UPJOHN AB
                                                           96US-00695692.
                                        96SE-00001245.
  97WO-SE000537
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                                                                                                                                           Hansson J,
Forsberg G;
                                                                                                                                                                                                      WPI; 1997-503052/46.
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                                                                                                                                           Antonsson P,
Abrahmsen L,
  26-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Staphylococcus enterotoxin SEE modified superantigen.
 20-APR-1998 (first entry)
 Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
                                                                                                                                                                                                                                                                                                                                                        The present sequence is the protein sequence of engineered staphylococcal superantigen SBAB-18. The superantigen is based on staphylococcal enterotoxin E (SBE, see ABPS8456) except for 4 amino acid residues close to the N-terminal that were from enterotoxin A and one substitution in the C-terminal part, D227A. Models of new superantigen variants were constructed using the SBA/B-18 model as the template. These include the new engineered superantigen SBA/B-120 (see ABPS455), which has been genetically fused to the Fab moiety of the tumour reactive antibody 5T4 to form a conjugate (see ABPS8454) polypeptide. The conjugate is a claimed example of novel conjugates of the invention comprising an engineered bacterial superantigen and an antibody moiety. The conjugates are designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prosetate (claimed)
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                        Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour; cytostatic; vaccine; SEA/E-18; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1210; DB 6; Length 233;
Pred. No. 4.6e-113;
1; Mismatches 4; Indels (
 Engineered superantigen SEA/E-18 for human cancer therapy
                                                                                                                                                                                                                        Walse
                                                                                                                                                                                                                         Antonsson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW35375 standard; peptide; 245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.78;
                                                                                                                                                 19-JUN-2002; 2002WO-SE001188.
                                                                                                                                                                         28-JUN-2001; 2001SE-00002327
                                                                                                                                                                                                                         Erlandsson E,
                                                                                                                                                                                                (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 228; Conservative
                                                                                                                                                                                                                                                 WPI; 2003-201467/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                           Staphylococcus sp
                                                                                                WO2003002143-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 233 AA;
                                                                                                                                                                                                                         Forsberg G,
                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                               structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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ID AAW3
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AC AAW3
XX
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AAW35375

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This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
type SEE superantigen is modified to be used in a novel conjugate. The
novel conjugate comprises a target seeking modety and a modified wild
type superantigen. This modified superantigen retains its ability to
activate a subset of T cells, even though l or more wild-type amino acid
activate in at least I region which functions in determining binding to T
cell receptor (TCR) and activation of a subset of T cells has/have been
replaced. Such a modified superantigen can optionally be used as part of
a conjugate with a target seeking moiety, for activating the immune
system to treat a mammalian disease. A pharmaceutical composition can be
prepared comprising a modified antibody (preferably a Fab fragment fused
c special moiety providing activation of T cells in Obera specific
c manner) in which cysteines providing for interchain cysteine linkages in
the native antibody have been replaced (preferably by serine residues) to
c prohibit cysteine formation. The modified wild-type superantigen is used
for treating cancer, viral infections, parasitic infestations and
autoimmune disease. The modified wild type superantigen has a lower
immunogenicity and reactivity with neutralishing antibodies and has fewer
immunogenicity and reactivity with neutralishing antibodies and has fewer
immunogenicity and eactivity with neutralishing antibodies and has fewer
cide-effects when used as a drug, compared to wild type superantigen.

Note: This sequence is not provided in the specification. It has been
created by modifying the wild-type SEE superantigen in Pages 38-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugate of target seeking molety and modified superantigen - useful for activating the immune system to treat cancer, viral infections, parasitic infestations and autoimmune diseases.
SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment; cancer; infection; autoimmune disease; antibody; modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1202; DB 2; Length 245;
Pred. No. 3.2e-112;
1; Mismatches 3; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dohlsten M, Kalland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= R27K
/note= "wild-type Arg is replaced by Lys"
                                                                                                                                                                                                                                                                                                                     'note= "wild-type Arg is replaced by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "wild-type Asn is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= S24G
/note= "wild-type Ser is replaced by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bjoerk P,
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PHAA ) PHARMACIA & UPJOHN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96SE-00001245.
96US-00695692.
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                                                                                                                                                                                                                                                                                /label= R20G
                                                                                                                                                                                                                                                                                                                                                                                                    label= N21T
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Best Local Similarity 93.5%;
Matches 229; Conservative
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Forsberg G;
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                                                                                                                       Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                               Misc-difference 21
                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antonsson P,
Abrahmsen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1997;
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181 RGLIVPHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNK-----TINSENLHIDL 228
                                                                                                                                                                                                                                                                                     Superantigen, SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; tumour associated lipid; anergy; T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
                                   120
                                                    61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
                                                                      EEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                9
                 9
         HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNBKAITENKESDDQFLENTLLFKGPFTG
                                                                                                                                                                                                                                                                   S. aureus SEE (staphylococcus enterotoxin E) protein.
                                                                                                                                                                                                               ABU79072 standard; protein; 248 AA.
                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2001; 2001US-00870759
                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2000; 2000US-0208128P
                                                                                                                                                                                                                                                   18-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (TERM/) TERMAN D S.
                                                                                                                                                                 241 YLYTT 245
                                                                                                                                               YLYTT 233
                                                                                                                                                                                                                                                                                                                                                    US2002177551-A1.
                                                                                                                                                                                                                                                                                                                APC; antitumour.
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                                                                                                                                                                                                                                 ABU79072;
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                                                                                                                                                                                             RESULT 9
ABU79072
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useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which computed immunocyte population, and administering the tumouricidally cumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidally activated imministering APC contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population contact T cells, in which adaptor proteins, which inhibit T cell contact T cells, in which adaptor proteins, which inhibit T cell cativated to produce a tumouricidally activated or functionally deactivated or functionally cativated or functionally cativated or functionally cativated T cells to the host, or allowing a superantigen-lipid raft to contact T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and caministering the tumouricidally activated T cells ex vivo, and caministering the tumouricidally activated T cells ex vivo, and caministering the tumouricidally activated T cells ex vivo, and caministering the tumouricidally activated or produce a cumouricidal or contact manneal (by allowing a tumour associated antigen to contact immunocytes in which adaptor to contact contact immunocytes in vivo. The cumouricidal T cell population in vivo in a mammal (contact defended or functionally descrivated) and manneal comparitions are useful for tractions with an entered or functions and compositions are useful for reapto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 BEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at "seqdata.uspto.gov/sequence.html?DocID=2002017751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcal enterotoxin E polypeptide seq id 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 248 AA;
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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (ARCS). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or sialylated glycans, useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis

T cells and antigen presenting cells.

라유

N-PSDB; ACA64698.

Disclosure; Page; 167pp; English.

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Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs) which may be used in the methods of the invention for treating cancer in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEEINEKDLRKKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 XVXXBKWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SEEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKVQRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                        further
                   'note= "Given in the specification as J, no further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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                                                                          ав J,
                                                                                                                               ò
                                                                                                                                                                                    /note= "Given in the specification as details given"
                                                                                                                             /note= "Given in the specification details given"
                                                                        'note= "Given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%; Score 1179; DB 2, 96.1%; Pred. No. 6e-110; iive 3; Mismatches 6
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                                       details given"
                                                                                              details given"
                                                                                                                                                                                                                                                                                                                        93WO-US005213
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nes 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stone JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-405418/50.
 Misc-difference 120
                                                                                                                                                                                                                                                                                                                                                                                                 TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                    (STON/) STONE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 230 AA;
                                                                                                                                                                     Misc-difference
                                                       Misc-difference
                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                      01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                           01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002
                                                                                                                                                                                                                                               WO9324136-A1
                                                                                                                                                                                                                                                                                   09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Terman DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB76235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BXXXXXB
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of an entrotoxin superantigen polypeptide the DNA encoding which can be transfected in to a cell alone or with DNA encoding a cell surface moiety to generate antitumour immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 SEKSEEINEKDLRKKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                    New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.0%; Score 1188; DB 7; Length 248; 100.0%; Pred. No. 8.2e-111; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL 224
                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 16; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR45012 standard; protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal enterotoxin SEE.
                                                                                                                                                                     99US-0173371P
                                                                                                                               28-DEC-2000; 2000US-00751708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                   WPI; 2003-787326/74.
                                                                                                                                                                                                      (TERM/) TERMAN D S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 248 AA;
                                                       US2003157113-A1
                   Staphylococcus.
                                                                                                                                                                     28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
08-JUN-1994
                                                                                            21-AUG-2003
                                                                                                                                                                                                                                               Terman DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR45012;
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Disclosure; Fig 2; 17pp; English
                                                                                         19-DEC-2000; 2000US-00741503
                Staphylococcus aureus
                                                                                                                                                  WPI; 2002-415198/44.
                                                    Misc-difference 124
                                                            Misc-difference 125
                                            Misc-difference 123
                                                                                                                                                                                                                                                                Sequence 230 AA;
                           Misc-difference
                                    Misc-difference
                                                                        US2002051765-A1
                                                                                                                                  (TERM/) TERMAN
                                                                                                     17-JAN-1990;
                                                                                                         17-JAN-1991
                                                                                                                          19-JUN-1995
                                                                                                 03-OCT-1989
                                                                                                                 02-MAR-1993
                                                                                                                      31-JAN-1994
                                                                                 02-MAY-2002
                                                                                                                                                                                                                                                                         Query Match
        therapy
                                                                                                                                           Terman
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DS;

US.

90US-00466577. 91WO-US000342. 92US-00891718.

93US-00025144. 94US-00189424. 95US-00491746.

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64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
                             121 XVXXXKWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEE. Synthetic polypeptides having structural homology to staphylococcal exctoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211
64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YNDLLVDKGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SEEINEKDIRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEEINEKDLRKKSELQRNALSNLRQIYYYNEKAKTENKESHDQFLQHTILFKGFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKVQRGL
                                                                                            124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions.
                                                                                                                                                                                         233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 230;
                                                                                                                                                                                       184 IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1156; DB 2;
Pred. No. 1.2e-107;
6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer treatment; pyrogen; tumouricide.
                                                                                                                                                                                                                                                                                                                                                        AAR13204 standard; protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcal enterotoxin E.
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Best Local Similarity 93.9%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-237984/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9110680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ß;
                                                                                                                                                                                                                                                                                                                                                                                                       AAR13204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Terman
                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                     AAR13204
                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8,8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the protein sequence of enterotoxin E (SEE) of Staphylococcus aureus. Similarity is shown, in several stretches of sequence, between staphylococcal enterotoxins, streptococcal pyrogenic exotoxins and staphylococcal exfoliative toxins (see ABB76214-44). In the present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive T and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B, and to streptococcal pyrogenic exotoxins, with statistically significant sequence homology and anilarity (2 value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding 6) to include alignment of cysteine residues and similar hydropathy profiles. These superantigens are used to treat solid tumours, including their metastases, without radiation, surgery or standard chemotherapeutic agents. A claimed method of human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        one or more superantigens ex vivo to generate stimulated cells, selecting a specific V beta subset of cells, and reintroducing these cells into the patient to induce an in vivo therapeutic, tumouricidal reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment involves contacting haematopoietic cells from a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                             Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reagent for treating cancer without the need for e.g. radiotherapy, comprises a specific V beta subset of T cells sensitized to a growing tumor and stimulated with superantigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SEEINEKOLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 230;
                                                                                                                                                                                                                                                                                                                                  in the specification"
                                                                                                                                                                                                                                                                                                                                                                                 in the specification"
                                                                                                                                                                                            in the specification"
                                                                                                                                                                                                                                                                                    in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 94.9%; Score 1175; DB 5; al Similarity 96.1%; Pred. No. 1.5e-109; 221; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                        in the
                                                                                                                                                                                            'note= "given as 'J'
                                                                                                                                                                                                                                                                                                                                  'note= "given as 'U'
                                                                                                                                                                                                                                                                                                                                                                                 /note= "given as 'V'
                                                                                                                                                                                                                                        "given as 'J'
                                                                                                                                                                                                                                                                                      'note= "given as 'O'
                                                                                                                                           Location/Qualifiers
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Gaps

63 9

183 120

Best Local Matches 22

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The present sequence is the protein sequence of engineered staphylococcal superantigen SEA/E-120. The superantigen is derived from staphylococcal enterotoxin E (SEE) by the incorporation of the following amino acid substitutions to reduce seroreactivity whilst maintaining production levels and biological activity: R206, N21T, S246, R27K, K79E, K81E, K81S and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the tumour reactive antibody 5T4 to form a claimed conjugate (see ABPS8454) designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
                                                                                                                                                                                                                  Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour; cytostatic; vaccine; SEA/E-120; mutant; mutein.
               233
IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                                                                                                                                                                                       Engineered superantigen SEA/E-120 for human cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                              Gly"
                                                                                                                                                                                                                                                                                                                                                                 'note= "wild-type Asn substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "wild-type Arg substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "wild-type Asp substituted by Ser"
                                                                                                                                                                                                                                                                                                                                    /note= "wild-type Arg substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "wild-type Lys substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type Lys substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                      þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                              /note= "wild-type Ser substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "wild-type Lys substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "wild-type Lys substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antonsson P,
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                  æ
                                                                                                  ABP58455 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 2; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2002; 2002WO-SE001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2001; 2001SE-00002327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erlandsson E,
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-201467/19.
                                                                                                                                                                                                                                                                                                                     Misc-difference 20
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 84
                                                                                                                                                                                                                                                                Staphylococcus sp
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                          14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forsberg G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure.
                                                                                                                                                                                                                                                                               Synthetic
184
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                                                                                                                                                                                                                                                                                                                     121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                                                                                                                  1 SEKSEEINEKDLRKKSELQCTALGNLKQIYYYNSKAITSSEKSADQFLTNTLLFKGFFTG
                                                                                                                                                                                                                                                                                          61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                              1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour; cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type Ser substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "wild-type Ile substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "wild-type Arg substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "wild-type Ser substituted by Gly"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild-type His substituted by Pro"
                                                                                                                            15; Indels
                                                                          Length
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1700cs "C242 constant heavy chain"

226. .458

/notes "SEA/E-120"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engineered superantigen for human cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "5T4 variable heavy chain"
                                                                       Score 1107; DB 6;
Pred. No. 1.1e-102;
                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                          89.4%;
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                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 245
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                                                                                                Local Similarity
les 209; Conserv
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                        Sequence 233 AA,
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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Region
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                                                                                                                               Matches
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Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
                                              note= "wild-type Phe substituted by Ser"
                                                                 'note= "wild-type Thr substituted by Lys"
                                                                                                        note= "wild-type Phe substituted by Leu"
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                                                                                                                                               'note= "wild-type Leu substituted by
                                                                                     note= "wild-type Ile substituted by
                                                                                                                            'note= "wild-type Thr substituted by
                                                                                                                                                                  'note= "wild-type Leu substituted by
                                                                                                                                                                                                                                                                                                         'n
         "wild-type Asp substituted
                                                                                                                                                                                      /note= "C242 constant light chain"
                            'note= "5T4 variable light chain"
                                                                                                                                                                                                                                                                                                          Walse
                                                                                                                                                                                                                                                                                                         Antonsson P,
                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 10; 102pp; English
                                                                                                                                                                                                                                                19-JUN-2002; 2002WO-SE001188
                                                                                                                                                                                                                                                                  28-JUN-2001; 2001SE-00002327
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                                                                                                                                                                                                                                                                                      (ACTI-) ACTIVE BIOTECH AB
                    . 565
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                                     Misc-difference 469
                                                                                                                                                         542
                                                         Misc-difference 504
                                                                                               Misc-difference 532
                                                                                                                  Misc-difference 536
 Misc-difference 452
                                                                                                                                     Misc-difference 537
                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                               structure.
                                                                                                                                                                                                                                                                                                          Forsberg
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The present sequence is a conjugate of a bacterial superantigen and an antibody moiety, and has been designed to target and destroy cancer cells. The bacterial superantigen is SEA/E-120 (see also ABPS8455), which was derived from staphylococcal enterotoxin E (SEB) by the incorporation of the following amino acid substitutions to reduce seroreactivity whilst constraining production levels and biological activity: R20G, N31T, S24G, R27K, K79E, K81E, K83S and D22/S. SEA/E-120 was genetically fused to the Fab moiety of the tumour reactive antibody 574. Substitutions were made in the 574 sequence to obtain higher yields: in the heavy chain, H41P, S44G, 1697 and V113G; and in the light chain, F10S, T45K, 163S, F73L, T77S, L78V and L83A. An expression vector comprising DNA encoding the conjugate can be used to transform host cells for recombinant production of the conjugate is useful for treating cancer, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,

Sequence 672 AA;

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                                                                                             HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                 9
                                                              1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                        Gaps
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 Length 672;
                        15; Indels
89.4%; Score 1107; DB 6;
89.7%; Pred. No. 4.9e-102;
ive 9; Mismatches 15;
                         Matches 209; Conservative
             Best Local Similarity
                                                                        226
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  Query Match
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121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEA. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See also AAR13204-R13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEA was isolated and purified from S.aureus. It can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                         RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                            233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions.
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82.8%; Pred. No. 1.9e-95;
tive 17; Mismatches 23;
                                                                                                                                                                                                                                                             SEA; cancer treatment; pyrogen; tumouricide.
                                                                                                                                              AAR13203 standard; protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 74pp; English
                                                                                                                                                                                                                                 Staphylococcal enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                            90US-00466577
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                                                                                                                                                                                                      (first entry)
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Best Local Similarity 82.8
Matches 193; Conservative
                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1990;
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                                                                                                                                                                                                                                                                                                                                                 25-JUL-1991.
                                                                                                                                                                                                      15-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the protein sequence of staphylococcal enterctoxin A (SEA). The invention provides movel conjugates (see ABP58454) for human cancer therapy. These comprise an engineered bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an antibody molety, such as tumour reactive antibody 574. Bacterial modelling of the engineered superantigens. The superantigens were engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The novel conjugates were designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEKSEEINEKDLRKKSELORNALSNIRQIYYYNEKAITENKESDDOFLENTLLFKGPFTG
                                                                                                                                                        Superantigen; staphylococcal enterotoxin A; antibody; cancer; tumour; cytostatic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
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82.0%; Pred. No. 3e-94;
ive 17; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                          Walse
                                                                                                                                                                                                                                                                                                                                                                                                          Erlandsson E, Antonsson P,
                              ABP58458 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 3; 102pp; English.
                                                                                                                             Staphylococcal enterotoxin A.
                                                                                                                                                                                                                                                                                                           19-JUN-2002; 2002WO-SE001188
                                                                                                                                                                                                                                                                                                                                           28-JUN-2001; 2001SE-00002327
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                         (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-201467/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                           Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 233 AA;
                                                                                                                                                                                                                                          WO2003002143-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          Forsberg G,
                                                                                             14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191;
                                                                                                                                                                                                                                                                            09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                             ABP58458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
RESULT 17
                ABP58458
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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RESULT 18

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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise activity. The peptides of the invention (AAU12559-AAU14009) comprise the peptide of Delta Peptide corresponds to amino acids 619-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-LIAI. The invention also relates to a method of identifying compounds that inhibit the corresponds to amethod of identifying compounds that inhibit the corresponds to distrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, peptides sequence from Staphylococcus aureus enterotoxin A represents a peptide sequence from Staphylococcus aureus enterotoxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07/DP178 complex, especially compounds with antifusogenic, antiviral intracellular modulatory activity, by detecting the formation of a
                                                                                                                                                     Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 BEKKVPINLWLDGKÓNTVPLETVKTNKKNVTVÓELDLÓARRYLOBKYNLYNSDVFDGKVÓ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or disrupts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.6%; Score 1023; DB 4; Length 257; 82.0%; Pred. No. 3.5e-94; ive 17; Mismatches 25; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                 Peptide sequence from Staphylococcus aureus enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Merutka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a compound that inhibits the formation of DP107/DP178 complex, especially compounds with antifue
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawless MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 42; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Erickson JB,
AAU14104 standard; peptide; 257 AA.
                                                                                                                                                                                                                                                                                                                            05-JUL-2000; 2000WO-US035727.
                                                                                                                                                                                                                                                                                                                                                                  99US-00350841.
                                                                                                                                                                         antiviral, HIV transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 82.0%
Matches 191; Conservative
                                                                           (first entry)
                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lackey JW,
                                                                                                                                                                                                                                                                                                                                                                                                      (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP107/DP178 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442157/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 257 AA;
                                                                                                                                                                                                                                                   WO200151673-A2
                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
                                                                           21-NOV-2001
                                                                                                                                                                                                                                                                                      19-JUL-2001.
                                     AAU14104;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Jeffs P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180 145 EEKKVPINLWLDGKONTVPLETVKTNKKNVTVOELDLOARRYLQEKYNLYNSDVFDGKVQ 204

121

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233

205 RGLIVEHTSTEPSVNYDLFGAQQQYSNTLLRIYRDNKTINSENWHIDIYLYTS 257

RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT

181

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Inhibiting transmission of Epstein-Barr virus to a cell, by contacting the cell with a peptide consisting of a region of Epstein-Barr virus
                                                         HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
Epstein-Barr virus infection; heptad repeat motif.
                                                                                                                                                                                         Petteway SR;
ABO10269 standard; protein; 257 AA.
                                                                                                                                                                                                                                                    Example; Fig 42; 716pp; English.
                                                                                                                                          93US-00073028.
94US-00255208.
94US-00360107.
                                                                                                                             95US-00485546
                             (first entry)
                                            S. aureus enterotoxin A.
                                                                                                                                                                                         Lambert DM,
                                                                                 Staphylococcus aureus.
                                                                                                                                                                          (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                        WPI; 2003-465599/44.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 257 AA;
                             19-AUG-2003
                                                                                               US6518013-B1
                                                                                                                             07-JUN-1995;
                                                                                                                                            07-JUN-1993;
                                                                                                                                                           20-DEC-1994;
                                                                                                              11-FEB-2003.
                                                                                                                                                                                         Barney SO,
              ABO10269;
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The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective virus to a cell, comprising contacting the cell with an effective concentration of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALMOTIS, comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carboxyl group, hydrophobic group or macromolecular carrier group, and Z comprises a carboxyl group, and group, hydrophobic group, or macromolecular carrier group, and fusion of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 clantified by analysing the structure/motifs present in the HIV-1 clantified by analysing the structure/motifs present in the HIV-1 containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues.

The method is useful for inhibiting transmission of Epstein-Barr virus in a cell and Epstein-Barr virus infection. The present sequence is a cell and experient from a pathogenic organism analysed for regions analogous to ö 9 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG Gaps .; 0 82.6%; Score 1023; DB 6; Length 257; 82.0%; Pred. No. 3.5e-94; ive 17; Mismatches 25; Indels Best Local Similarity 82.08 Matches 191; Conservative Query Match

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120

84

25 61 85

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HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT

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The invention relates to novel oligonuclectide primers directed against enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable enterotoxin gene (yst) of bacteria Yersinia enterocolitica. The novel oligonuclectide primers are useful for simultaneously detecting food poisoning bacterial species Staphylococcus aureus and/or Yersinia enterocolitica in food systems e.g., milk, fruit juices and ice creams, without prior enrichment for preventing food poisoning outbreak. The PCR detection method is useful for detecting the bacteria strains in quantity as low as one cell. The method can be directly used for detecting bacterial strains. The oligonuclectide primers allow quick and highly sensitive detection of the food poisoning bacterial species. This sequence represents the protein derived from the enterotoxin A gene from Staphylococcus aureus of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                 enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 SEKSEEINEKDERKKSELQGTALGALLKQIYYYNEKAKTENKESHDOFLQHTILFKGFFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel oligonucleotide primers directed against enterotoxin A gene of Staphylococcus aureus and heat stable enterotoxin gene of Yersinia enterocolitica, useful for detecting food poisoning causing bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                Staphylococcus aureus enterotoxin A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 191; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 14-15; 34pp; English
                                   ADD44368 standard; protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      (COUL ) COUNCIL SCI & IND RES
                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002; 2002WO-IB001150.
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002; 2002WO-IB001150.
                                                                                                            (first entry)
                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-779273/73.
N-PSDB; ADD44369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 257 AA;
                                                                                                                                                                                                                                                                                    WO2003080865-A1.
                                                                                                          15-JAN-2004
                                                                                                                                                                                                                                                                                                                        32-OCT-2003
                                                                                                                                                                                                           ice cream
                                                                         ADD44368;
RESULT 20
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A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738) superantigen. Nucleic acids encoding superantigens (see also AAW06737, AAW06739), esp. truncated forms of the superantigen lacking the leader peptide, can be used in the gene therapy of cancer, infectious diseases and immunological disorders. The nucleic acid, optionally in combination with cytokine or chemokine nucleic acids, is delivered to an animal using e.g. liposomes. It acts by controlling the activity of effector cells, such as T-cells, macrophages, monocytes and/or natural killer cells. Localised prodn. Of an effective but non-toxic amount of encoded proteins allows safe treatment of the animal
                                                                                                                                                                                                                                                                                                                                               Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell; lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 EKKVPINLWLDGKQNTVPLETVKTNKGNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTLFKGFFTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant molecule encoding super:antigen and opt. cytokine or chemokine - controls activity of effector cells (T cells, monocytes, natural killer cells), used for gene therapy of cancer.
                          181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.3%; Score 1019; DB 2; Length 233; 81.9%; Pred. No. 7.7e-94; ive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 98-99; 131pp; English
                                                                                                                                                            AAW06738 standard; protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potter TA;
                                                                                                                                                                                                                                                                                                      Staphylococcus enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00446918.
95US-00580806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US007432
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elmslie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-011857/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT45699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1995;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9636366-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1996;
                                                                                                                                                                                                                                                        08-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1996
                                                                                                                                                                                                          AAW06738;
                                                                                                                                                                                                                                                                                                                                                                                                    adjuvant.
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                                                                                                                                         AAW0673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for computational design and selection of protein binding peptides, comprising computing the hydrophobic potential of all surface points arranged on the solvent contact surface of a protein three-dimensional structure, developing a two-dimensional characteristic map by a self-assembly method, identifying a region of hydrophobic amino acids by Fourier transformation and designing a protein binding peptide corresponding to the hydrophobic region. The method is useful for designing and selecting protein binding peptides. This sequence represents an Enterotoxin A protein used in the scope of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Designing and selecting protein binding peptide by identifying peptide binding region of protein, and designing peptides that bind to the region using structure-biological activity relationship program of computer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                        145 EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVPDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYGCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEKSEEINEKDLRKKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterotoxin A; Computational design; protein binding peptide; hydrophobic potential; solvent contact surface; protein three-dimensional structure; two-dimensional characteristic map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                   205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257
                                                                                         181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.6%; Score 1023; DB 8; Length 257;
82.0%; Pred. No. 3.5e-94;
ive 17; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; SEQ ID NO 1; 11pp; Japanese.
                                                                                                                                                                                                                                                      ADH10956 standard; protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ENKA-) ENKAKU IRYO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002; 2002JP-00062348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2002; 2002JP-00062348
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fourier transformation
                                                                                                                                                                                                                                                                                                                                                                                             Enterotoxin A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-075279/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ses 191; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2003263465-A.
                                                                                                                                                                                                                                                                                                                                                  11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2003
121
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Matches
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comprising administering to a subject an overlapping synthetic peptide formulation (OSPP) which comprises a combination of single chain peptides corresponding to the amino acid sequence of a protein of interest. The method of the invention has immunostimulant, virucide, antibacterial, antiparasitic and cytostatic applications and may be useful during vaccine production and for treating immune disorders including viral, bacterial and parasitic infections, prion diseases, neoplastic diseases, as well as providing protection against toxins. The current sequence is that of the OSPF-related Staphylococcus aureus enterotoxin A protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g an immune response, useful for treating immune disorders, e.g. cterial and parasitic infections, prion diseases, or neoplastic administering to a subject an overlapping synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for modulating an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                     immune response; overlapping synthetic peptide formulation; OSPF; immunostimulant; virucide; antibacterial; antiparasitic; cytostatic; vaccine; viral; bacterial; parasitic infection; prion disease;
182 GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                    Length 233;
                                                                                                                                                                                                                                    OSPF-related Staphylococcus aureus enterotoxin A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.3%; Score 1019; DB 8;
81.5%; Pred. No. 7.7e-94;
ive 18; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID NO 226; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                           ADI95318 standard; protein; 233 AA
                                                                                                                                                                                                                                                                                                                             neoplastic; toxin; enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-2003; 2003WO-US020322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-2002; 2002US-0392718P.
                                                                                                                                                                                                  (first entry)
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Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral, bacterial and
diseases, administeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-082868/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    WO2004002415-A2.
                                                                                                                                                                                                04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruprecht RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Formulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating
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This is the wild-type Staphylococcus enterotoxin SEA superantigen. This SEA superantigen can be modified to be used in a novel conjugate. The convel conjugate comprises a target seeking moiety and a modified wild type superantigen. The modified superantigen retains its ability to activate a subset of T cells, even though lor more wild-type amino acid residues in at least 1 region which functions in determining binding to T cellareceptor (TCR) and activation of a subset of T cells has/have been crepaced. Such a modified superantigen can optionally be used as part of a conjugate with a target seeking moiety, for activating the immune cystem to treat a mammalian disease. A pharmaceutical composition can be prepared comprising a modified antibody (preferably a Fab fragment fused to peptide moiety providing activation of T cells in Wheta specific to a peptide moiety providing activation of T cells in Wheta specific to a peptide moiety providing activation of T cells in Wheta specific to prohibit cysteine formation. The modified wild-type superantigen is used for treating cancer, viral infections, parasitic infestations and autoimmune disease. The modified wild type superantigen has a lower immunogenicity and reactivity with neutralising antibodies and has fewer cimmunogenicity and reactivity with neutralising antibodies and has fewer side-effects when used as a drug, compared to wild type superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conjugate of target seeking moiety and modified superantigen - useful for activating the immune system to treat cancer, viral infections, parasitic infestations and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                     SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment; cancer; infection; autoimmune disease; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                181 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKSINSENWHIDIYLYTS
RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.1%; Score 1016; DB 2; Length 233; 81.5%; Pred. No. 1.5e-93; ive 17; Mismatches 26; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalland T;
                                                                                                                                                                                                                                                                   Staphylococcus enterotoxin SEA wild-type superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bjoerk P, Dohlsten M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 36-37; 58pp; English
                                                                                                                                           AAW35373 standard; peptide; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96SE-00001245.
96US-00695692.
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Matches 190; Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hansson J,
Forsberg G;
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                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                              WO9736932-A1
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Abrahmsen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                         20-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1997.
  181
                                                                                                                                                                                   AAW35373;
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                                                                                                     RESULT 24
                                                                                                                          AAW35373
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9 9 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD

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121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

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Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune diseases.
                 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which may be used in the methods of the invention for treating cancer in a patient. These SEs, and homologues of them, can be used as tumouricidal aperts for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEKSEBINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLXHTILFKGFFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                       181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 233;
                                                                                                                                                                                                                                                                                               enterotoxin; SE; cancer; tumouricidal agent;
                                                                                                                                                                                                                                                                                                              autoimmune disease; toxicity; Protein A; perfusion system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
81.8%; Score 1013; DB 2; Length 2
Best Local Similarity 81.5%; Pred. No. 3.1e-93;
Matches 190; Conservative 16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                              'note= "Given in the specification as
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 90pp; English.
                                                                                                                                                                       AAR45011 standard; protein; 233
                                                                                                                                                                                                                                                                       Staphylococcal enterotoxin SEA
                                                                                                                                                                                                                                                                                                                                                                                                            details given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93WO-US005213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-00891718.
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stone JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-405418/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STON/) STONE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 233 AA;
                                                                                                                                                                                                                                                                                               Staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9324136-A1
                                                                                                                                                                                                                              25-MAR-2003
08-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perman DS,
                                                                                                                                                                                                  AAR45011;
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                                                                                                                                           RESULT 2
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a tumour cell capable of stimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule fabra activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an anticancer immune response in vivo or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGFPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor cell capable of stimulating antitumor immune reactivity in vitro o in vivo comprises exogenous nucleic acids encoding a superantigen and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1016; DB 4; Pred. No. 1.5e-93 17; Mismatches 2
                                                                                                                                                                                                                                                                                  Staphylococcus aureus enterotoxin A protein.
                                                                                                                                                                                                                                                                                                               Tumour; cancer; immune; enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 16pp; English
                                                                                                                                                                                              AAB67338 standard; peptide; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91WO-US000342.
92US-00891718
93US-00025144.
94US-00189424.
95US-00491746.
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90US-00466577.
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81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00183437.
                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 81.59
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               costimulatory molecule
                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                    US6180097-B1
                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-1998;
                                                                                                                                                                                                                                                        23-APR-2001
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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCB).

Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in a mammal companient of the producing (M1) a tumouricidal limpids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, cancer comprising alalylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted, a construct useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by cancer treatment associated lipids are inactivated or deleted to produce a superantigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superantigen, SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; tumour associated lipid; anergy; T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic; APC; antitumour.
EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.
                                             RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                  S. aureus SEA (staphylococcus enterotoxin A) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                      ABU79068 standard; protein; 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2001; 2001US-00870759
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N-PSDB; ACA64694.
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121
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ABU79068
ID ABU79068
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population ex vivo in a mammal) by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell cativated to tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host, treating caministering the tumouricidally activated T cells to the host, treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a tumouricidal T cell population ex vivo in a mammal comprising allowing a tumouricidal T cell population ex vivo in a mammal comprising allowing a cumcentigen-lipid raft conjugate to contact immunocytes in vivo. The receptors methods and compositions are ob-administered or administered as functions and compositions are co-administered or administered as fusion constructs with anti-tumour proteins or motife. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EBKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKVQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 SEKSEBINEKDLRKKSBLQGAALGNLKQIYYYNEKAKTENKESHDQFLQHTLLFKGFFTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; Staphylococcal enterotoxin A; SEA; enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 RGLIVEHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENWHIDIYLYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.8%; Score 1013; DB 6; Length 257; Best Local Similarity 81.5%; Pred. No. 3.6e-93; Matches 190; Conservative 17; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segdata.uspto.gov/sequence.html?DocID=20020177551"
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Staphylococcus sp.
Synthetic.
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                                          (TERM/) TERMAN
          31-JAN-1994;
02-MAR-1993;
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                                                                rerman DS;
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Matches
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                                                                                                        The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of an entrotoxin superantigen polypeptide the DNA encoding which can be transfected in to a cell alone or with DNA encoding a cell surface moiety to generate antitumour immunity.
                                                                                                                                                                                                                                                                                                                                   61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                 85 HSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
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                                                                                                                                                                                                                                                                                                                                                                                            145 EEKKVPINLWLDGKQNTVPLETVKTNKRONTVQELDLQARRYLQEKYNLYNSDVPDGKVQ 204
                                                                                                                                                                                                                                                                                        1 SEKSEEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                      for
                                                                                                                                                                                                                                                                                                      25 SEKSEEINEKDLRKKSELQGAALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
                                         New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                           81.8%; Score 1013; DB 7; Length 257;
81.5%; Pred. No. 3.6e-93;
ive 17; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "amino acid residue given as
                                                                                     Example 3; SEQ ID NO 8; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB76234 standard; protein; 233
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90US-00466577.
91WO-US000342.
92US-00891718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification
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                                                                                                                                                                                                                                                       Best Local Similarity 81.5*
Matches 190; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
                    WPI; 2003-787326/74.
                                                                                                                                                                                                                        Sequence 257 AA;
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17-JAN-1990;
17-JAN-1991;
01-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB76234;
                                                                                                                                                                                                                                              Query Match
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Staphylococcus aureus. Similarity is shown, in several stretches of sequence, between staphylococcal enterotoxins, streptococcal pyrogenic excutants and staphylococcal excotoxins, streptococcal pyrogenic excotoxins and staphylococcal excotoxins, streptococcal pyrogenic present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive T and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B, and to streptococcal pyrogenic exctoxins, with statistically significant sequence homology and similarity (Z value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding 6) to include alignment of cysteine residues and similar hydropathy profiles. These superantigens are used to treat solid tumours, including their metasteases, without radiation, surgery or strandard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one or more superantigens ex vivo to generate stimulated cells, selecting a specific V beta subset of cells, and reintroducing these cells into the patient to induce an in vivo therapeutic, tumouricidal reaction
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                                                                                                                                                                                                                                                                                                                                                                        Reagent for treating cancer without the need for e.g. radiotherapy, comprises a specific V beta subset of T cells sensitized to a growing tumor and stimulated with superantigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
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81.1%; Pred. No. 2.5e-92;
tive 16; Mismatches 28;
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94US-00189424.
95US-00491746.
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189; Conserv
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205 RGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS

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'note= "wild-type Leu substituted by Arg" 'note= "wild-type Asp substituted by Arg" /note= "wild-type Tyr substituted by Ala"

/label= Mature protein . .25 /label= Signal_peptide location/Qualifiers

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The present sequence is the protein sequence of staphylococcal enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine comprises 3 amino acid substitutions introduced into the SEA sequence: Comprises 3 amino acid substitutions reduce the binding of the toxin to major histocompatibility complex (MHC) Class II and/or T cell receptors. The full-length expressed product is secreted into the periplasmic space of Escherichia coli host cells, and the leader peptide is recognised and cleaved by a native mechanism. The vaccine is used to protect against upperantigen toxin infections. Superantigen attributes are absent, but the superantigen toxin infections. Superantigen toxins were shown to protect animals appropriate antibody response is produced. In examples from the invention, attenuated superantigen toxins were shown to protect animals invention, attenuated superantigen toxins were shown to protect animals the altered superantigen toxins as vaccines, and in diagnosis and the altered superantigen toxins as vaccine consisting of altered to provide protective immunity against the majority of bacterial superantigen toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Col 33-35; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                   (USSA ) US SEC OF ARMY
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                                                                                                                                      Misc-difference 94
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                                                                                                                                                                                                                                                                                               01-SEP-1998;
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                  Key
Peptide
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Bavari

Olson MA,

98US-00144776 97US-00882431

ö HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120 144 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180 9 84 85 HSWYNDLLVRFDSKDIVDKYKGKKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 25 SEKSEBINEKDLRKKSBLQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTD SEKSEEINEKDLRKKSELORNALSNLROIYYYNEKAITENKESDDOFLENTLLFKGFFTG Gaps RGLIVEHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233 ö Length 257; 28; Indels Query Match

80.8%; Score 1000; DB 5;
Best Local Similarity 80.7%; Pred. No. 7.2e-92;
Matches 188; Conservative 17; Mismatches 28; Sequence 257 AA; 61 121 145 181 셤 g ð 유 ઠે ઠે

The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of staphylococcal enterotoxin New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial Enterotoxin A; superantigen-associated bacterial infection; vaccine; Claim 10; Page 18-19; 50pp; English. ABU10081 standard; protein; 257 AA Bavari S; Staphylococcal enterotoxin A #1 97US-00882431. 97US-00882431. (first entry) Ulrich RG, Olson MA, WPI; 2003-401542/38. N-PSDB; ACA61177. ULRI/) ULRICH R G. superantigen toxin (OLSO/) OLSON M A. (BAVA/) BAVARI S. Staphylococcus sp. US2003009015-A1. Sequence 257 AA; 25-JUN-1997; 25-JUN-1997; 11-AUG-2003 09-JAN-2003. infection ABU10081;

ö 120 144 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180 9 84 1 SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 85 HSWYNDLLVRFDSKDIVDKYKGKKVDLYGAYAGYQCAGGTPNKTACMYGGYTLHDNNRLT 25 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTILFKGFFTD Gaps ö Length 257; Indels 80.8%; Score 1000; DB 6; 80.7%; Pred. No. 7.2e-92; 17; Mismatches Best Local Similarity 80.7 Matches 188; Conservative Query Match 셤 ઠ g 8 g Š

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                               SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; antibacterial.
                      RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Wild-type Leu substitued by Glu"
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                                                                                                                                                                                                                                                                                        S. aureus periplasmic enterotoxin A mutant #1
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'label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                   ABU62324 standard; protein; 257
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98US-00144776
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                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is a protein related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                      25 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTD 84
1. Also disclosed are mutated staphylococcal enterotoxin A, B, Cl (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the LASELA8R/DYOR/Y896/Y92A (with reference to the mature protein sequence) mutant of periplasmic SEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for preparing a composition infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                      SEKSBEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RGLIVPHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 257;
                                                                                                                                                                                                                                                                                                                                             28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superantigen toxin; vaccine; infection; gene therapy
                                                                                                                                                                                                                                                                             80.8%; Score 1000; DB 7;
80.7%; Pred. No. 7.2e-92;
iive 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      superantigen toxin DNA fragment, treating or preventing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein #1 related to the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2001; 2001WO-US046540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                          Local Similarity
es 188; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD56764.
                                                                                                                                                                                                                       Sequence 257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003056015-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invention
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Sequence 257 AA;

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WPI; 2002-546281/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                    attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6399332-B1
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                                                                                                                                                                                                                                                                              182
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                                                                                                                         Query Match
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                                                                                                                         EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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Staphylococcus aureus which causes gastrointestinal distress, or toxic
                                                         HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                               SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                             Gaps
                                                                                                                                                               RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                          Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine; Venezuelan equine encephalitis virus; vaccine vector; vaccine; Staphylococcal intoxication; Staphylococcus exotoxin.
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                                                                                                                                                                                                                                                                                          Amino acid sequence of a mutant Staphylococcal enterotoxin A.
           Length 257;
                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
           DB 7;
           Score 1000; DB 7;
Pred. No. 7.2e-92;
17; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Glu encoded by AGAA"
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                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Ser encoded by
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Misc-difference 2
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                                                                                                                                                                                                                                 AAY54463 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith JF,
           80.8%;
80.7%;
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                                                                                                                                                                                                                                                                       25-APR-2000 (first entry)
                             188; Conservative
                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-160826/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pushko P,
                    Similarity
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N-PSDB; AAZ45833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shock syndrome.
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           Query Match
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                      Local
                            Matches
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  providing immunity tool for detection
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recombinant proteins produced are used as vaccines for providing immuni against Staphylococcal intoxication or as a diagnostic tool for detection of Staphylococcus excloxin. The transformed host cells are used to analyse the effectiveness of drugs and agents which inhibit S. aureus exotoxins or release of exotoxins. Infectious alpha-virus particles comprising the mutant SEA or SEB genes are used for providing immunity against Staphylococcal exotoxins by generating a protective immune reaction in humans or animals. The vaccines are used to reduce disease symptoms or reduce severity of disease caused by enterotoxins of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EKSEEINEKDLRKKSELQGTALGULKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKKVPINIMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, superantigen; antigen; toxin; vaccine; A489270C; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                            Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "wild-type Asp substituted by Arg"
                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild-type Tyr substituted
                                                                                                                                                                                                                                                                                                                                         80.5%; Score 996; DB 3;
80.6%; Pred. No. 1.6e-91;
ive 17; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB79502 standard; protein; 233 AA
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                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity ov.v
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                              Sequence 233 AA;
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97US-00882431.
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 25-JUN-1997;
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                                                                                                                                                                        infection
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ID ABU6
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                                                                                                      comprises 3 amino acid substitutions introduced into the SEA sequence:
1488, v89A and DOR. These mutations reduce the binding of the toxin to major histocompatibility complex (WHC) (1488 II and/or I cell receptors.
1488, v89A and DOR. These mutations reduce the binding of the toxin to major histocompatibility complex (WHC) (1488 II and/or I cell receptors.
15 The protein is expressed as a nonsecreted product within host Escherichia coli cells. The vaccine is used to protect against superantigen toxin infections. Superantigen attributes are absent, but the superantigen toxin infections is effectively recognised by the immune system and an appropriate antibody response is produced. In examples from the invention, attenuated superantigen toxins were shown to protect animals against challenge with wild-type toxin. Methods of producing and using the altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided. A selb, sec. 1, TSST-1 and streptococcal SPEa is predicted to provide selb, sec. 1, TSST-1 and streptococcal SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins
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                     Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                               2 EKSEBINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTILFKGFFTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                                                                                                                                  EKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                              staphylococcal
                                                                                                                                                                                                                                                                                                                               80.5%; Score 996; DB 5; Length 233; 80.6%; Pred. No. 1.6e-91; ive 17; Mismatches 28; Indels
                                                                                               The present sequence is the protein sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by AT"
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                                                                       Claim 5; Col 37-39; 46pp; English
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.6*
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus sp.
                                                                                                                                                                                                                                                                                                         Sequence 233 AA;
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The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or I cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EKSEEINEKDLRKKSELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.5%; Score 996; DB 6; Length 233; 80.6%; Pred. No. 1.6e-91; ive 17; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;

 S. aureus cytoplasmic enterotoxin A mutant #1.

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                                                                                                                     Bavari
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                                                                                                                  Ulrich RG, Olson MA,
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                                                                                                                                                                            WPI; 2003-401542/38.
(ULRI/) ULRICH R G.
                           (OLSO/) OLSON M A. (BAVA/) BAVARI S.
                                                                                                                                                                                                           N-PSDB; ACA61178
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by Gly"

"Encoded by ATGAG"

/note=

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The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MMC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cuperantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, of a mammal against superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. The superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin bNA fragment is useful for preparing and SPED). The superantigen toxin DNA fragment is useful for preparing and SPED). The superantigen toxin DNA fragment is a seful of or preparing and SPED).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for treating or preventing bacterial infection. The present
sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.5%; Score 996; DB 7; Length 233; 80.6%; Pred. No. 1.6e-91; ive 17; Mismatches 28; Indels
                                                                                                                                                                                   /note= "Wild-type Tyr substitued by Ala"
                                                                      "Wild-type Leu substitued by Arg"
                                                                                                         note= "Wild-type Asp substitued by Arg"
                                   "Wild-type Leu substitued
                                                                                                                                            /note= "Wild-type Tyr substitued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 24-25; 68pp; English
                                                                                                                                                                                                                                                                                                 26-NOV-2001; 2001US-00002784
                                                                                                                                                                                                                                                                                                                                    97US-00882431.
98US-00144776.
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                                                                        note=
                                     note=
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             (ULRI/) ULRICH R G
                                                    Misc-difference 48
                                                                                                                             Misc-difference 89
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                 Misc-difference
                                                                                       Misc-difference
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                                                                                                                                                                                                                        US2003036644-A1
                                                                                                                                                                                                                                                                                                                                      25-JUN-1997;
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122 EKKVPINLWLDGKQNTVPLETVKTNKKRNTVQELDLQARRYLQEKYNLYNSDVFDGKVQR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is a protein related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLPKGFFTGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                      Superantigen toxin; vaccine; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
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80.6%; Pred. No. 1.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 110-112; 141pp; English.
                                                                                                                                                                                                                                                                                           note= "Encoded by AT"
                                                                                                                                                                           Protein #2 related to the invention
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                        AAE37677 standard; protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001; 2001WO-US046540.
                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001; 2001US-00002784
                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD56765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                        WO2003056015-A1.
                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                06-OCT-2003
                                                                                                                                                                                                                                                                                                                                                    10-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ulrich RG;
                                                                                                                     AAE37677;
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or a biologically active fragment or bomologue frase fragment protein comprising the SAg or its fragment or selected from Staphylococcal enterotoxin. A Streptcoccal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin A (SEA) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEKSEBINEKDLRKKSELQGTA--GNKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superantigen; SAg; Staphylococcal enterotoxin; SE; SEA; cytostatic;
                                                                                                         GLIVEHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 991; DB 8; Length 231;
80.3%; Pred. No. 5e-91;
ive 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcal enterotoxin A (SEA) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1; 91pp; English.
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                                                                                                                                                                                                                                                                       ADF89824 standard; protein; 231
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28-AUG-2002; 2002US-0406697P.
29-AUG-2002; 2002US-0406750P.
01-OCT-2002; 2002US-0415310P.
02-OCT-2002; 2002US-0415400P.
09-UTM-2003; 2003US-0438686P.
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; cancer.
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                                                                                                                                                                                                               RESULT 40
ADF89824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or Leal antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host calls are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the staphylococcus enterotoxin A K14E mutant. Note: The present sequence is not present in the specification but was created by the indexer from the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKSEEINEKDLREKSELQGTALGNIKQIYYYNEKAKTENKESHDQFRQHTILFKGFFTDH
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                                                                                                                                                                                                                                                                    Enterotoxin A; superantigen-associated bacterial infection; mutant; superantigen toxin; vaccine; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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80.2%; Pred. No. 4e-91;
ive 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Lys susbstituted by Glu"
                                                                                                                                                                                                                     Staphylococcus enterotoxin A K14E substitution mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               staphylococcus enterotoxin A sequence (see ACA61178)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                       ABU10099 standard; protein; 233 AA.
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                                                                                                                                                                (first entry)
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Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olson MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OLSO/) OLSON M A. (BAVA/) BAVARI S.
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                                                                                                                                                                                                                                                                                                                                                     Staphylococcus sp.
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                                                                                                            ABU10099;
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  RESULT 39
                           ABU10099
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ARU10099
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ABU11-P
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ABU111-P
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ABU111-P
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New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
EEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompacibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the staphylococcus enterotoxin A Y64A mutant. Note: The present sequence is not present in the specification but was created by the indexer from the wild-type
                                                               Enterotoxin A; superantigen-associated bacterial infection; mutant; superantigen toxin; vaccine; mutein.
                                                                                                       RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
                                                                                                                        /note= "Wild-type Tyr susbstituted by Ala"
                                                                                                                                                                                                                                                                                               Staphylococcus enterotoxin A Y64A substitution.mutant
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers Misc-difference 64
                                                                                                                                                                                                            ABU10098 standard; protein; 233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page; 50pp; English.
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                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ULRI/) ULRICH R G.
(OLSO/) OLSON M A.
(BAVA/) BAVARI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-401542/38.
                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                           119
                                                                                                        181
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79.7%; Score 987; DB 6; Length 233;

staphylococcus enterotoxin A sequence (see ACA61178)

Sequence 233 AA;

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                                                                                                       121
                                                                                                                                     121
                                                                                                                                                                  181
                                                                                                                                                                                               181
                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superantigen toxin; SAg; Staphylococcal enterotoxin A; SEA; cytostatic; antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor; antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; treatment; superantigen-associated bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26. .253
/label= Mature Staphylococcal enterotoxin_A
/note= "Includes transcription start site residue, Met"
                                                                                                                       62 SWANDLLVRFDSKDIVDKYKGKKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                      62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE
                                                                                                                                                                                    122 EKKVPINLMEDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQR
                                                             2 EKSEEINEKDLRKKSELQGTALGULKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTDH
                                                                                                                                                                  BKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR
                                            2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.
                 Gaps
                                                                                                                                                                                                                                               182 GLIVPHTSTEPSVNYDLFGAQQQXSNTLLRIYRDNKTINSENMHIDIYLYTS 233
                                                                                                                                                                                                                            182 GLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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   Pred. No. 1.3e-90;
7; Mismatches 29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2. .25
/label= Leader_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcal enterotoxin A.
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   80.2%;
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                 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-224177/19.
N-PSDB; AAZ51105.
Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus sp.
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                  overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen- associated bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                               85 HSWYNDLLVRPDSKDIVDKYKGKKVDLYGAYAGYQCAGGTFNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                         EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                   25 SEKSEBINEKDLRKKSEKQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLLFKGFFTD 84
  specific antibodies. This vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superantigen toxin, SAg, Staphylococcal enterotoxin A, SEA, cytostatic, antibacterial, vaccine, MfC class II receptor; T-cell antigen receptor; antibody; toxxid; staphylococcal/streptococcal toxin; diagnosis; mutant; treatment; superantigen-associated bacterial infection; A489270P.
                                                                                                                                                                                                                                                            1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGPFTG
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .233
/label= Mature_Staphylococcal_enterotoxin_A
/note= "Mutant sequence without the leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
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                                                                                                                                                                             79.4%; Score 983; DB 3; Length 257; 79.8%; Pred. No. 3.7e-90; Live 17; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Wild type Leu substituted with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Wild type Tyr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcal enterotoxin A for vaccine A489270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Wild type Asp substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by CAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Encoded by TTG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Encoded by CTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Encoded by AG"
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SEA vaccines
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                                                                                                                                         Sequence 257 AA;
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hes 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKKVPINLWLDGKONTVPLETVKTNKKNVTVOELDKOARRYLOEKYNLYNSDVFDGKVAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                              The present amino acid sequence is the mutant Staphylococcal enterotoxin A (SEA), a bacterial superantigen toxin (SAg), used for the formulation of SEA vaccine A498270P. The coding region of this SAg toxin is altered by site directed mutagenesis, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. This altered SAg toxin has the leader peptide cleaved by native bacterial enzymatic mechanism and the first residue of the mature protein is encoded by the transcriptional start site (ATG). SEA has antibacterial and cytostatic activity. This sequence is useful for the production of SEA vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EKSEEINEKDLRKKSEKQGTALGNLKQIYYYNEKAKTENKESHDQFRQHTLFKGFFTDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                         Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superantigen; SAg; Staphylococcal enterotoxin; SE; SEJ; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amelioration of superantigen-associated bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.0%; Score 978; DB 3; Length 233; 79.3%; Pred. No. 1e-89; ive 17; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcal enterotoxin J (SEJ) superantigen.
                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 74-76; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
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                                                                     Bavari S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2003; 2003WO-US014381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                     Olson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; cancer.
                                                                                                                                             WPI; 2000-224177/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus sp
                                                                                                                                                                                    N-PSDB; AAZ51106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 233 AA;
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin J (SEJ) superantigen.
                                                                                                                                                                                                                                                    Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 12; 91pp; English
                                                    01-OCT-2002; 2002US-0415310P.
02-OCT-2002; 2002US-0415400P.
09-JAN-2003; 2003US-0438686P.
  2002US-0389366P
                    2002US-0406697P
                                                                                                                                                                                                                    WPI; 2004-011997/01
                                                                                                                                       (TERM/) TERMAN D S.
                    29-AUG-2002;
29-AUG-2002;
01-OCT-2002;
02-OCT-2002;
15-JUN-2002;
                                                                                                                                                                                 Terman DS
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Sequence 268 AA;

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WYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBE 122
                                                                                                                                           KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRG 182
                                                                                                                                                                                                        62
                                                                                           86
                                                                              27 KNETIKEKNLHKKSELSSITLANLRHIYFFNEKGISEKIMTEDQFLDYTLLFKSFFISHS
                                                            KSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHP
                                 Gaps
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                                                                                                                                                                                                                                                                   207 LIVPHTSKEPLVSYDLFNVIGQYPDKLLKIYQDNKIIESENMHIDIYLYTS 257
                                 ;
0
67.0%; Score 830; DB 8; Length 268; 64.9%; Pred. No. 9.9e-75; ive 38; Mismatches 43; Indels
                 Best Local Similarity 64.99
Matches 150; Conservative
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ABU79071 standard; protein; 258 AA
                    18-JUN-2003 (first entry)
             ABU79071;
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S. aureus SED (staphylococcus enterotoxin D) protein.

Superantigen: SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; tumour associated lipid; anergy; T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic; APC; antitumour

Staphylococcus aureus.

US2002177551-A1

28-NOV-2002.

30-MAY-2001; 2001US-00870759.

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S

Terman DS;

WPI; 2003-361759/34. N-PSDB; ACA64697.

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the creatment of cancer, which binds to tumour associated lipids and induces an arguer of cancer, which binds to tumour associated lipids and induces canery or apoptosis in the T cells and antigan presenting cells (APCe). Ago included are a mammalian cell useful in the treatment of cancer where the receptors which binds thours associated lipids and induces cellular inactivation or death is deleted or functionally deactivated composition as for immunosupersessive fatty acids, ceramides, juylycolphids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosids, sphingolipids, glycosphingolipids and proteogytoclipids are inactivated or caleted), a construct useful in the treatment of cancer comprising a subjace fatty acids, ceramides, juylycolphingolipids, useful in the treatment of cancer comprising a caleted in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or inhibits T cell activated), a composition useful in the treatment of cancer (where an adaptor protein which inhibits T cell activated), a composition was sociated lipid and the contact immunocyte population, and administering the tumouricidal immunocyte population, and administering the tumouricidal population, and administering the tumouricidal lipids are inactivated or deleted to produce a tumouricidal induced injude to contact produce a superantigen, to the host), producing (M) a tumouricidal lipid activated or deleted to produce a tumouricidal population, and administering the tumour associated lipids to contact paces, in which receptors for the thour associated lipids to contact call which adaptor proteins, and administering the tumouricidal population of contact calls in which adaptor proteins, and administering the tumouricidal population of contact minutoward call by administering a tumouricidal population in vivo in a mammal (My) administering the tumouricidal population in vivo in a mammal or contact stanhylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551" sequence represents a bacterial superantigen protein (e.g.

Sequence 258 AA;

Length '258; DB 6; 53.6%; Score 663;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of an enterotoxin superantisen polypeptide the DNA encoding which can be transfected in to a cell alone or with DNA encoding a cell surface moiety to generate antitumour immunity.
                                                                                                                                      86 LINFEDLLINFNSKEMAQHFKSKNVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNKLK 145
                                                                                                                                                                               EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                               61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                          9
                                                                            for
                                                         SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; Staphylococcal enterotoxin D; SED; enterotoxin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                            Gaps
                                                                                                                                                                                                                                                            206 RGKIEFDSSDGSKVSYDLFDVKGDPPEKQLRIYSDNKTLSTEHLHIDIYLY 256
                                                                                                                                                                                                                                          RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                            ö
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcal enterotoxin D polypeptide seg id 14.
   6e-58;
70;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 14; 151pp; English.
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                   Z
54.5%; PATE 35; 7
                                                                                                                                                                                                                                                                                                                                                 ADF43294 standard; protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000; 2000US-00751708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0173371P
                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2004 (first entry)
            Similarity 54.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-787326/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2003157113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1999;
                            126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DS;
                                                                                                                                                                                                                                                                                                                                                                              ADF43294;
                                                                                                                                                                                                              146
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                          Matches
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selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin D (SED) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                           86 LINFEDLLINFNSKEMAQHFKSKAVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNKLK 145
                                                                                               146 ERKKIPINLMINGVQKEVSLDKVQTDKKNVTVQELDAQARRYLQKDLKLYNNDTLGGKIQ 205
                                                                            EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
         HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                                                                                                                                                                                                                                                                                                                                                                                            Superantigen; SAg; Staphylococcal enterotoxin; SE; SED; cytostatic;
                                                                                                                                               RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                 DB 8; Length 258;
                                                                                                                                                                                                                                                                                                                                                                           Staphylococcal enterotoxin D (SED) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%; Score 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 6; 91pp; English.
                                                                                                                                                                                                                                                                      ADF89829 standard; protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2002; 2002US-0378988P.
15-UTW-2002; 2002US-038956EP.
28-AUG-2002; 2002US-0406697P.
29-AUG-2002; 2002US-0406750P.
01-6CT-2002; 2002US-041510P.
02-CCT-2002; 2002US-0415400P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2003; 2003WO-US014381
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-011997/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TERM/) TERMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003094846-A2
                                                                                                                                                                                                                                                                                                                                         26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terman DS;
                                                                                                                                               181
                                                                                                                                                                                                                                                                                                        ADF89829;
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                                                                                                                                                                                                                                                      ADF89829
                                                                                                                                                                                                                                    RESULT
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Gaps

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1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Query Match 53.6%; Score 663; DB 7; Length 258; Best Local Similarity 54.5%; Pred. No. 6e-58; Matches 126; Conservative 35; Mismatches 70; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEB) which may be used in the methods of the invention for treating cancer in a patient. These SEB, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
                                                               61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                         EEKKVPINLMIDGKOTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                          9
                                              85
                                        SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of staphylococcal enterotoxin(s) and homologues - for treating in a patient or for the treatment of auto-immune diseases.
                                                                                                                                 231
               ö
                                                                                                                                  RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY
                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                    stapnylococcal enterotoxin; SB; cancer; tumouricidal agent;
autoimmune disease; toxicity; Protein A; perfusion system.
               Indels
6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 657; DB 2;
Pred. No. 2e-57;
               Mismatches
       Pred. No.
                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 90pp; English.
                                                                                                                                                                                            AAR45013 standard; protein; 228
               35;
                                                                                                                                                                                                                                                      Staphylococcal enterotoxin SED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%;
                                                                                                                                                                                                                                                                                                                                                  93WO-US005213
                                                                                                                                                                                                                                                                                                                                                                  92US-00891718
      54.5%;
                                                                                                                                                                                                                                     (first entry)
               Matches 126; Conservative
                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                           Stone JL;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-405418/50.
                                                                                                                                                                                                                                                                                                                                                                                  TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                           STONE J L.
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                                 01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1992;
                                                                                                                                                                                                                                                                                                                WO9324136-A1
                                                                                                                                                                                                                            25-MAR-2003
08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                            Terman DS,
                                                                                98
                                                                                                                                                                                                            AAR45013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                 121
                                                                                                                                                  206
                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                  (TERM/)
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                                                                                                                                                                                   AAR45013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rumor cell capable of stimulating antitumor immune reactivity in vitro or
in vivo comprises exogenous nucleic acids encoding a superantigen and a
costimulatory molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP 126
                          INLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 INEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKEKELHKKSELSSTALNNMKHSYADKNPI I GENKSTGDOFLENTLLYKKFFTDLINFED
LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 228;
                                                                                                                                                                        187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67; Indels
                                                                                                                                                                                                 53.1%; Score 657; DB 4;
.larity 55.6%; Pred. No. 2e-57;
Conservative 33; Mismatches 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus enterotoxin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour; cancer; immune; enterotoxin.
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                                                                                                                                                                                                                                                                                                                               228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-00466577.
91WO-US000342.
92US-00891718.
93US-00025144.
94US-00189424.
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                                                                                                                                                                                                                                                                                                                               AAB67340 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-158657/16
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Matchès 125; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6180097-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                         AAB67340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                               62
                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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67; Indels

Mismatches

33;

Conservative

Local Similarity hes 125; Conserv

Best Loca Matches

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61

INEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND

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67; Indels

Length 228;

DB 5;

53.1%; Score 657; DB 5; 55.6%; Pred. No. 2e-57; ive 33; Mismatches 6

Query Match Best Local Similarity 55.67 Matches 125, Conservative

61

62 LLINFNSKEMAQHFKSKNVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNKLKERKKIP 121

. 69

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LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP

7 INEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND

122 INLWINGVQKEVSLDKVQTDKKOVTVQELDAQARRYLQKDLKLYNNDTLGGKIQRGKIBF

182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLY 226

187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY

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INLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF

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equence, between staphylococcal enterotoxins, streptococcal pyrogenic exotoxins and staphylococcal enterotoxins, streptococcal pyrogenic exotoxins and staphylococcal enterotoxins (see ABB76214-44). In the present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive T and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B, and to streptococcal pyrogenic excetoxins, with statistically significant sequence homology and similarity (Z value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding 6) to include alignment of cysteine residues and tumours, including their metastases, without radiation, surgery or standard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with come or more superantigens ex vivo to generate stimulated cells, selecting a specific V beta subset of cells, and reintroducing these cells into the patient to induce an in vivo therapeutic, tumouricidal reaction
                                                 186
122 INLWINGVQKEVSLDKVQTDKKAVTVQELDAQARRYLQKDLKLYNNDTLGGKIQRGKIEF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                   Enterotoxin D; SED; superantigen; antigen; tumour; cancer; antitumour;
                                                 INLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reagent for treating cancer without the need for e.g. radiotherapy, comprises a specific V beta subset of T cells sensitized to a growing tumor and stimulated with superantigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence of enterotoxin D (SED) Staphylococcus aureus. Similarity is shown, in several stretches of
                                                                                                                  231
                                                                                                                                    187 HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY
                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus enterotoxin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 2, 17pp, English.
                                                                                                                                                                                                                                ABB76236 standard; protein; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900S-00466577.
91WO-US000342.
92US-00891718.
93US-00025144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00741503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00491746
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-415198/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002051765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000;
                                                                                                                                                                                                                                                                                                   09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Terman DS;
                                                                                                                                                 182
                                                                                                                                                                                                                                                                   ABB76236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SED. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SED was isolated and purified from S.aureus. It can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 INEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Treating cancer with enterotoxin from Staphylococcus aureus -administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%; Score 649; DB 2; Length 228; 55.1%; Pred. No. 1.3e-56; ive 33; Mismatches 68; Indels
                                                                                                                                                   SED; cancer treatment; pyrogen; tumouricide.
                              ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 74pp; English.
                            AAR13205 standard; protein; 228
                                                                                                                                                                                                                                                                           90US-00466577.
                                                                                                                                                                                                                                                                                                        90US-00466577.
                                                                                                                      Staphylococcal enterotoxin D.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 124; Conservative
                                                                                                                                                                                  Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-237984/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                       US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                       (TERM/) TERMAN
                                                                                                                                                                                                                                                                           17-JAN-1990;
                                                                                                                                                                                                                                                                                                        .7-JAN-1990;
                                                                                        15-OCT-1991
                                                                                                                                                                                                              WO9110680-A.
                                                                                                                                                                                                                                                                                                                                                                     Terman DS;
                                                         AAR13205;
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Best Local S
RESULT 51
                AAR13205
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Sequence 228 AA;

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Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 DDWKKDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGGATNKTQCSYGGVTLSDNNKYD 140
                 108 IGVQKEVSLDKVQTDKKAVTVQELDAQARRYLQKDLKLYNA-----IQRGKLEFDSAAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein, useful as a vaccine for treating or infection, specifically an infection caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG
GSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVPINLWI
                                                                                                                                                                                                                                                                                                                                                            Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to novel genes and encoded proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                       STVSYDLFDAQGQYPDTLLRIYRDNKTINSBNLHIDLYLY 231
                                                                                                                                        39.8%; Score 492.5; DB 6; 39.8%; Pred. No. 8.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 396; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scarselli M;
                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus protein #198
                                                                                                                                                                                                                                    ABM70958 standard; protein; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Staphylococcus aureus
preventing Staphylococcal
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.8'
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-120786/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 250 AA;
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 72
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                                                                                                                                                                                                        RESULT 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
                                                                                             186
                                                53
    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody moiety, such as tumour reactive antibody 574. Bacterial enterotoxins such as SEA, SEE, SED and SEH were used in the molecular modelling of the engineered superantigens. The superantigens were engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The novel conjugates were designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDL
   VKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTDLINFED
                                                                                             INLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF
                                                                                                                                                                                                                                                                                                                                                                                           Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour; cytostatic; vaccine.
                                LLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the protein sequence of staphylococcal enterotoxin D (SED). The invention provides novel conjugates (see ABPS8454) for human cancer therapy. These comprise an engineered bacterial superantigen, such as novel SEA/E-120 (see ABPS8455), an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%; Score 523; DB 6; Length 203; 49.5%; Pred. No. 5.2e-44;
                                                                                                                                                           HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                             DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Mismatches
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                                                                                                                                                                                                                                                                      ABP58459 standard; protein; 203 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2001; 2001SE-00002327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forsberg G, Erlandsson E,
                                                                                                                                                                                                                                                                                                                                                                  Staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ACTI-) ACTIVE BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-201467/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 203 AA;
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                                                                62
                                                                                             127
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                                                                                                                                                                                                                                                                                                   ABP58459;
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Matches
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61 KTACMYGGVTLHDNNRLTEEKK 82

ABU62338 standard; protein; 82 AA.

RESULT 55 ABU62338

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The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the superantigens to MHC class II or T-cell antigen receptors. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                       Superantigen-associated bacterial infection; superantigen toxin; vaccine;
SEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                               198 KGYVKYYNDDEONVEYDFYNLNGEYGREVLKMYADNKTINSDKLHLDIXLF 248
                                                                                                                                    181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
36.9%; Score 457; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.3e-38;
Matches 82; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 ABU10091 standard; protein; 82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 36; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial superantigen toxin SEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bavari S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00882431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-401542/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OLSO/) OLSON M A. (BAVA/) BAVARI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003009015-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1997;
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121
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                                                                                                                                                                                                                                                                                                         RESULT 54
ABU10091
XX
ABU10091
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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHZ class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, an infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an treating/ameliorating a superantigen-associated bacterial infection, and treating/ameliorating a superantigen-associated bacterial infection, and anithody which recognises altered TSST-1. Superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the S. aureus enterotoxin B, SEB, MHC binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                           SEE; staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.9%; Score 457; DB 7; Length 82 100.0%; Pred. No. 6.3e-38; ive 0; Mismatches 0; Indel8
                                                                                                              S. aureus enterotoxin E, SEE, MHC binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KTACMYGGVTLHDNNRLTEEKK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 68pp; English
                                                                                                                                                                                                                                                                                                                                                    26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                         97US-00882431.
98US-00144776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%;
                                                                         (first entry)
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Matches 82, Conservative
                                                                                                                                                                                                                                   Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ULRI/) ULRICH R G.
                                                                                                                                                                                                                                                                          JS2003036644-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82 AA;
                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                               31-SEP-1998;
                                                                         27-AUG-2003
                                                                                                                                                                                                                                                                                                               30-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ulrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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KTACMYGGVTLHDNNRLTEEKK 124

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RESULT 56 ABU10089

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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or Teall antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin peptide, diagnosing superantigen toxin for producing antigent cond immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an example required from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin and an antibody which recognises and series of SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 399; DB 7; L. Pred. No. 4.3e-32; 4; Mismatches 7;
                                        S. aureus enterotoxin A, SEA, MHC binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 3; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTACMYGGVTLHDNNRLTEEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24299 standard; protein; 91
                                                                                                                                                                                                                                                                                                     2001US-00002784.
                                                                                                                                                                                                                                                                                                                                             97US-00882431.
98US-00144776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%;
86.6%;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.2
Best Local Similarity 86.6
Matches 71; Conservative
                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                            ULRI/) ULRICH R G.
                                                                                                                                                                                                                  US2003036644-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82 AA;
                                                                                                                               antibacterial.
                                                                                                                                                                                                                                                                                                     26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                               25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 58.....
  27-AUG-2003
                                                                                                                                                                                                                                                          20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ulrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW24299;
SAKKEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating euperantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the bacterial superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN 102
                                                                                                                                                                                                                                        Superantigen-associated bacterial infection; superantigen toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHDQFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 399; DB 6; Length 82; Pred. No. 4.3e-32; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 35; 50pp; English
                                                                     ABU10089 standard; protein; 82 AA.
                                                                                                                                                                                                Bacterial superantigen toxin SEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bavari S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00882431
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                                                                                                                                                        11-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 86.6
les 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-401542/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ULRI/) ULRICH R G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLSON M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAVA/) BAVARI S.
                                                                                                                                                                                                                                                                                                                                                    US2003009015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82 AA;
                                                                                                                                                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     5-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ulrich RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin SEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection
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                                                                                                             ABU10089;
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Length 82; Indels 9

14-APR-1998 (first entry)

ABU62336 standard; protein; 82 AA.

Best Loca Matches

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ABU62336

RESULT 57
ABU62336
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AC ABU6
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Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 DLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINL 129
                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence of staphylococcal entertoxin D (SED). The invention provides movel conjugates (see ABPS454) for human cancer therapy. These comprise an engineered bacterial superantigen, such as novel SEA/E-120 (see ABPS455), and an antibody moiety, such as tumour reactive antibody 574. Bacterial enterotoxins such as SEA, SEE, SED and SEH were used in the molecular modelling of the engineered superantigens. The superantigens were engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The novel conjugates were designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SE KFATADLAQKFKUKUVUJYGASFYYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 WIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 KDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superantigen; SAg; Staphylococcal enterotoxin; SE; SEH; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 EGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL-HIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
                                                                                                                                          Walse B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcal enterotoxin H (SEH) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.6%; Score 366; DB 6; 37.9%; Pred. No. 3.6e-28; tive 46; Mismatches 81.
                                                                                                                                          Antonsson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF89833 standard; protein; 217 AA
                                                                                                                                                                                                                                                                                                                                Example 3; Fig 3; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2003; 2003WO-US014381.
                   19-JUN-2002; 2002WO-SE001188.
                                                          28-JUN-2001; 2001SE-00002327.
                                                                                                                                          Erlandsson E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                   (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                 WPI; 2003-201467/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003094846-A2
                                                                                                                                          Forsberg G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                           structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF89833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a novel polypeptide, which is optionally expressed in NCIMB 40771. The polypeptide, and polymcideotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds that bind and inhibit the activity of the polypeptide. Such compounds can be used as anti-bacterial compounds. The polypeptide may also be used as an immunogen to vaccinate an animal for protection against Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MYGGVTLHDNNRLTEEKKVPINLWLDGKXNTVPLETVKTNKKONVTVQELDLQARRYLQEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Staphylococcus aureus polynucleotide and polypeptide(s) - for isolating antagonist of the polypeptide(s) useful as anti-bacterials
                                    Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen; vaccine; disease; protection; isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 370; DB 2; Length 91;
Pred. No. 4.2e-29;
Mismatches 13; Indels
Staphylococcus aureus Gene #5 polypeptide sequence 2
                                                                                                                                                                                   /note= "Unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 FGLYNSDSFGGKVQRGLIVFHSSEGSTVSYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 33; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP58460 standard; protein; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal enterotoxin H.
                                                                                                                                                                                                                                                                                                               97WO-GB000524
                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham MKR, Hodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aureus caused disease
                                                                                                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-435166/40.
N-PSDB; AAV01865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus sp
                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 91 AA;
                                                                                                                                                                                                                                                                                                             25-FEB-1997;
                                                                                                                                                                                                                            WO9731114-A2
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                                                                                                                                                                                                                                                                   28-AUG-1997
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Gaps

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homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfixingens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, perioardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin H (SEH) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 DLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVPINL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 WIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| | : ::|:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 KOLRKKSELORNALSNIRQIYYYNEKAITENKESDDOFLENTLIFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superantigen; SAg; Staphylococcal enterotoxin; SE; SEI; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to treating a subject with cancer. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.6%; Score 366; DB 8; Length 217; 37.9%; Pred. No. 3.6e-28; rive 46; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcal enterotoxin I (SEI) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 10; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF89834 standard; protein; 242 AA
                                                                                                                      2002US-0406750P.
2002US-0415310P.
2002US-0415400P.
                                                            2002US-0389366P.
2002US-0406697P.
                                                                                                                                                                                                                    09-JAN-2003; 2003US-0438686P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-011997/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus sp
                                                                                                                                                                                                                                                                                        (TERM/) TERMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 217 AA;
                                                                                                                      29-AUG-2002;
01-OCT-2002;
02-OCT-2002;
                                                            15-JUN-2002;
28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                            Terman DS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF89834
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WO2003094846-A2.

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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, perioardial effusion or meningal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin I (SEI) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVPINLWIDGKQTTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK------VQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 VGNLRNFYTKHDY1DLKGVTDKNLP1ANQLE-----FSTG---TNDLISESNNWDEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 KFKGKKLDIFGIDYNGFC-----KSKYMYGGATL-SGQYLNSARKIPINLWVNGKHKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superantigen; SAg; Staphylococcal enterotoxin; SE; SEL; cytostatic; gene therapy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.4%; Score 339.5; DB 8; Length 242; 35.6%; Pred. No. 2e-25; ive 36; Mismatches 74; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 HSSEGSTVSYDLFDAOGOYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcal enterotoxin L (SEL)superantigen.
                                                                                                                                                                                                                                                                                                                                                                 a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 11; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF89837 standard; protein; 240 AA
                                                                                                  2002US-0389366P.
2002US-0406697P.
2002US-0406750P.
                                                                                                                                                   01-0CT-2002; 2002US-0415310P.
02-0CT-2002; 2002US-0415400P.
09-JAN-2003; 2003US-0438686P.
                                                  08-MAY-2003; 2003WO-US014381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.6°
Matches 79; Conservative
                                                                                                                                                                                                                                                                                               WPI; 2004-011997/01.
                                                                                                                                                                                                                            (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 242 AA;
                                                                                                                                    29-AUG-2002; 2
01-OCT-2002; 2
02-OCT-2002; 2
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Streptococcus polypeptide SEQ ID NO 7890
                                                                                                WO200234771-A2
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Tettelin H;
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Best Local S
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  셤
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to treating a subject with cancer. The method cinvolves administering an amount of a superantisen (SAG) composition comprising a molecule selected from: a native SAG protein; its biologically active fragment or a biologically active fragment or a biologically active fragment or biologically active fusion protein comprising the SAG or its fragment or homologue tused to a fusion partner polypeptide or peptide. The SAG is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, perioardial effusion or meningeal carcinomatosis. The present sequence
                                                                                                                                                                                                                                                                                Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 YKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TKSVSTDKKAVTAQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSSKFYSGFDKGSVVFH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 IDKVKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 NLRNFYTKYEYVNLKAVKDKAVSPESHRLE------YSYKADTLYAEFDNEYITSD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 NLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LLVDLGSKDATNK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a Staphylococcal enterotoxin L (SEL) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 337; DB 8; Length 240; 35.3%; Pred. No. 3.5e-25; ative 37; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 14; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP29357 standard; protein; 259
                                                                                                         08-MAY-2002; 2002US-0378988P.
15-JUN-2002; 2002US-0389366P.
28-AUG-2002; 2002US-0406697P.
29-AUG-2002; 2002US-0406750P.
01-CCT-2002; 2002US-0415400P.
02-OCT-2003; 2003US-0415400P.
09-JAN-2003; 2003US-0438686P.
                                                                                     08-MAY-2003; 2003WO-US014381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                          MPI; 2004-011997/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 78; Conserv
                                                                                                                                                                                                            (TERM/) TERMAN D S
             Staphylococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 240 AA;
                                    WO2003094846-A2
                                                           20-NOV-2003
                                                                                                                                                                                                                                    Terman DS;
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Matches
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ABP29357
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AC ABP2
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the gpecification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I), may be used to treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ---KQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ELQRNALSNIRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYN---DLLVDLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 GNIIFHLNSGERISYNLFDTGHGDRESMLKKYSDNKTAYSDQLHIDIYL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani V, Margarit Y RosI, Grandi G, Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 336.5; DB 5; Length 259; 33.6%; Pred. No. 4.4e-25; Live 44; Mismatches 85; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3920; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001WO-GB004789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-352536/38.
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fragment or a biologically active fragment or proposition or peptide. The SAg is homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin M (SEM) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 HAVDVYGLSYSGYCL----KNKYIYGGVTL-AGDYLEKSRRIPINLWVNGEHQTISTDK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFHSSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 NLRN--YYGSYPIEDHQSINPENNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 NLRQIYYYNEKAITENK--ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
                                                                                                                                                                   Superantigen; SAg; Staphylococcal enterotoxin; SE; SEM; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%; Score 320; DB 8; Length 239; 33.0%; Pred. No. 1.8e-23; ive 40; Mismatches 78; Indels 2
                                                                                                                                 Staphylococcal enterotoxin M (SEM) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 15; 91pp; English
                   ADF89838 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2002; 2002US-0378988P.
15-JUN-2002; 2002US-0389366P.
28-AUG-2002; 2002US-0406697P.
29-AUG-2002; 2002US-0406750P.
01-OCT-2002; 2002US-0415310P.
02-OCT-2002; 2003US-0415400P.
09-JAN-2003; 2003US-0415400P.
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                                                                                            26-FEB-2004 (first entry)
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Matches 72; Conservative
                                                                                                                                                                                         gene therapy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-011997/01
                                                                                                                                                                                                                              Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TERM/) TERMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239 AA;
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                                                       ADF89838;
ADF89838
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fragment or a biologically active fragment or protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin G (SEG) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 KGK-----KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a subject with cancer or malignant diseases comprises oral, intrathecal or intracavitary administration of an amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 NLRQIY --YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 NIRNFYANYQPEKLQGVSSGNFSTSHQLE---YIDGKYTLYSQFH------NEY
                                                                                                                                                                                                                                             Superantigen; SAg; Staphylococcal enterotoxin; SE; SEG; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
             194 GSSFSYDLFDTGTGQAESFLKIYNDNKTVETEKFHLDV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%; Score 319.5; DB 8; 33.8%; Pred. No. 2e-23; ive 35; Mismatches 71;
                                                                                                                                                                                                                 (SEG) superantigen.
191 GSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating a subject with cancer or malignan intratumoral, intrathecal or intracavitary a superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9; 91pp; English
                                                                                                               ADF89832 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0389366P.
2002US-0406697P.
2002US-0406750P.
2002US-0415310P.
2002US-0415400P.
                                                                                                                                                                                                                   Staphylococcal enterotoxin G
                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2003; 2003WO-US014381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-2003; 2003US-0438686P
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Best Local Similarity 33.8%
Matches 76; Conservative
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-011997/01.
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                                                                                                                                                                                                                                                                                                     Staphylococcus sp.
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28-AUG-2002;
29-AUG-2002;
01-OCT-2002;
02-OCT-2002;
                                                                                                                                                                                  26-FEB-2004
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                                                                                                                                                 ADF89832;
                                                                                RESULT 65
                                                                                                 ADF89832
                                                                                                                                   셤
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80 9/ us-09-900-766-7.rag

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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAG) composition comprising a molecule selected from: a native SAG protein; its biologically active fragment or a biologically active homologue or a biologically active fragment or a biologically active fragment or bonologue tused to a fusion protein comprising the SAG or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAG is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exocoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, accites, pericardial effusion or meningeal carcinomatosis. The present sequence
                                     Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of a superantigen composition to the subject.
   ----SDSFGGKVQRGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superantigen; SAg; Staphylococcal enterotoxin; SE; SEK; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a Staphylococcal enterotoxin K (SEK) superantigen.
                                                                                                                                             IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                  TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcal enterotoxin K (SEK) superantigen.
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                                                                                                                                                                                                                                                                                                                                                                                           ADF89836 standard; protein; 242 AA
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15-UTV-2002; 2002US-0389366P.
28-MUG-2002; 2002US-0406637P.
29-AUG-2002; 2002US-0406750P.
01-GCT-2002; 2002US-0415310P.
02-GCT-2002; 2002US-0415400P.
09-JAN-2003; 2003US-0415400P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003094846-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2004
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                                                                                                                                             184
                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF89836;
136
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29 IDNLRNFYTKKDFINLKDVKDN----DTPIANQLQF----SNESY-DLISESKDFNKFS 78 LSNLRQIY----YYNEKAITENKESDDOFLENTLLFKGFFTGHPWYNDLLVDLGSKDAIN 78

25.0%; Score 310; DB 8; Length 242; 33.2%; Pred. No. 1.8e-22; ive 39; Mismatches 76; Indels 34;

Conservative

74;

23

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Similarity

Local Matches

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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCS).

Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (ML) a tumouricidal immunocyte oppulation in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which cereptors for immunosupressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, shalylated glycans, lipopeptides and proceeglycolipids, gangliosides, sialylated glycans, lipopeptides and proceeglycolipids are inactivated cleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nuclectide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which the treatment of cancer (where an adaptor protein which the inhibite T cell activation by tumour associated antigens is deleted or the interface or the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; tumour associated lipid; anergy; T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
                                                                                                                                                   functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidal APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis
                                  79 KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV
                                                                                                                       139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VQRGLIVF
                                                                                                                                                                                                                                           187 HSSEGSTVSYDLF-DAOGOYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                    192 HLNNNDŤFSYDĽFYTGDDGLPKSFĽKÍYEDNKTVESEKFHĽDV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. aureus SEB (staphylococcus enterotoxin B) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in T cells and antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU79069 standard; protein; 266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2001; 2001US-00870759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2000; 2000US-0208128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-361759/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACA64695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APC; antitumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2003
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contact APCs, in which reapples for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal) by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating contact in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour adsociated lipids in vivo), producing (MS) carcer in a mammal contact immunostytes in which adaptor trumour associated antigens are deleted or functionally deactivated) and producing (M7) a cumouricidal T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a tumouricidal T cell activation ex vivo in a mammal comprising allowing a tumouricidal T cell population ex vivo in a mammal comprising allowing a tumouricidal T cell activation ex vivo in a mammal and producing and an expectated or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing and producing producing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at sequence.html?DocID=20020177551"
population ex vivo in a mammal (by allowing a tumour associated lipid to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present
              888888888888888888888888888888888
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Sequence 266 AA;

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-----AGGTPNKTACMYGG 110
                                                                                                                                                                               VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                         171 NSDSFGGKVORGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                  85 LGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 144
                                                                               1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                Gaps
                               19;
24.3%; Score 300.5; DB 6; Length 266; 33.6%; Pred. No. 1.9e-21; Live 47; Mismatches 96; Indels 19.
                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC----
                  Best Local Similarity 33.6
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                       YLYT 232
                                                                                                                                                                                                                                                                                                                                     YLTT 263
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      Query Match
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Enterotoxin B; SEB; immunomodulatory; IgE antibody; atopic eczema; lupus erythematosus; Crohn's disease; multiple sclerosis; psoriasis; rheumatoid arthitis; immunoglobulin E; dermatological; antiasthmatic; antiallergic; ophthalmological; antiposoriatic; antirheumatic; antiarthritic; neuroprotective; immunosuppressive; antiinflammatory; vasotropic; antidiabetic; thyromimetic; antibacterial; gynaecological;
                              ABG75015 standard; protein; 266 AA
                                                                                                                                             S aureus enterotoxin B protein.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                cytostatic
                                                                      ABG75015;
RESULT 68
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202

232

YLYT

229

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Staphylococcus aureus enterotocin B (EBB) protein. These peptides are capable of binding to immunoglobulin (1g) E antibodies. However, unlike SEB, they do not induce proliferation of T cells. The peptides are useful as immunomodulators and inhibitors of exterior production in T cells, particularly for treatment of atopic eczema, bronchial asthma, allergic rhinoconjunctivitis, psoriasis, rheumatoid arthritis and multiple sclerosis and for inducing or strengthening the Thi/Th2 immune responses, specifically for treating psoriasis, autoimmune uveitis, allergic contact eczema, Behcet's syndrome, diabetes mellitus, Hashimoto's thyroiditis, infection by Helicobacter pylori, lupus erythematosus, Crohn's disease, multiple sclerosis, organ transplant rejection, rheumatoid arthritis and spontaneous, recurrent abortion. They can also be used, in vitro, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 BFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibiting IFNgamma production and for modulating spontaneous or
stimulated cytokine production in Th1/Th2 cells. The present sequence is
the SEB protein as used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG
                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide that binds immunoglobulin E and alters cytokine synthesis, useful for treating e.g. atopic eczema, asthma or allergy, also its encoding nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to novel peptides derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Score 300.5; DB 7;
33.6%; Pred. No. 1.9e-21;
tive 47; Mismatches 96;
                                                 1. .27
/label= signal_peptide
                                                                                  28. .266
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 43-44; 46pp; German.
                                 Location/Qualifiers
                                                                                                                                                                                                       14-FEB-2003; 2003WO-EP001511.
                                                                                                                                                                                                                                       2002DE-01007734.
2002DE-01040866.
                                                                                                                                                                                                                                                                                           (AGEL-) AGELAB PHARMA GMBH.
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 Staphylococcus aureus.
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nes 82; Conserv
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                                                                                                                                   WO2003068812-A2.
                                                                                                                                                                                                                                       15-FEB-2002;
04-SEP-2002;
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                                                 Peptide
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AAW06737 standard; protein; 255 AA.
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                                                                08-MAR-1997
                                                                                                                                                                                                                                                                                   18-MAY-1995;
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                                         AAW06737;
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Best Local S
                                                                                                                               adjuvant
                                                                                                                                                                                   Peptide
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RESULT 70
          AAW06737
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                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of an enterotoxin superantigen polypeptide the DNA encoding which can be transfected in to a cell alone or with DNA encoding a cell surface moiety to generate antitumour immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Gaps
                                                                                                       receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; Staphylococcal enterotoxin B; SEB; enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.3%; Score 300.5; DB 7; Length 266; 33.6%; Pred. No. 1.9e-21; ive 47; Mismatches 96; Indels 19.
                                                                                   Staphylococcal enterotoxin B polypeptide seg id 10.
                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 10; 151pp; English
                   ADF43290 standard; protein; 266 AA.
                                                                                                                                                                                                                                        99US-0173371P
                                                                                                                                                                                                                   28-DEC-2000; 2000US-00751708
                                                              12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.63
Matches 82; Conservative
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                                                                                                                                                                                                                                                             (TERM/) TERMAN D S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 YLTT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 266 AA;
                                                                                                                                                                       US2003157113-A1.
                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                        28-DEC-1999;
                                                                                                                                                                                             21-AUG-2003
                                                                                                                                                                                                                                                                                   Terman DS;
                                        ADF43290;
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                                                        Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell; lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A CDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC------AGGTPNKTACMYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant molecule encoding super:antigen and opt. cytokine or chemokine - controls activity of effector cells (T cells, monocytes, natural killer cells), used for gene therapy of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.2%; Score 300; DB 2; 34.0%; Pred. No. 2e-21; iive 46; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 96-97; 131pp; English
                                                                                                                                                                                                                                                                          1. .15
/label= Sig_peptide
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potter TA;
   œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00446918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US007432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        safe treatment of the animal
Staphylococcus enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elmslie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-011857/01.
N-PSDB; AAT45698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                               Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAOGOYPD--TLLRIYRDNKTINSENLHIDLY

232

230 LYT

TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN

171

59 GNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGV 118

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RESULT 72
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:: | | | : | | | : | | | | | | | | | EFNN--SPYETGYIKPIENENS-FWYDWMPAPGDKFDQSKYLMMYNDNKOVDSKDVKIEV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin B (SEB) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superantigen; SAg; Staphylococcal enterotoxin; SE; SEB; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 299.5; DB 8; Length 238; 33.7%; Pred. No. 2.1e-21; ive 46; Mismatches 96; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcal enterotoxin B (SEB) superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 2; 91pp; English.
                                                                                                                                                                                                                                                                                                                                  ADF89825 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002; 2002US-0406750P.
01-0CT-2002; 2002US-0415110P.
02-0CT-2002; 2002US-0415400P.
09-JAN-2003; 2003US-0438686P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2003; 2003WO-US014381.
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2002US-0406697P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; cancer.
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                                                                                                   YLYT 232
                                                                                                                                                                    YLTT 252
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28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
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                                     192
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                                                                                                   229
                                                                                                                                                                 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                           Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity; toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor; therapeutic; vaccine; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide(s) derived from pyrogenic exotoxin - useful for, e.g. antagonising toxin-mediated activation of T cells and prevention or treatment of toxic shock caused by exotoxin(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.2%; Score 299.5; DB 2
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96
                                                                                       AAW64647 standard; peptide; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 41; 68pp; English
                                                                                                                                                                                               Synthetic SEB protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96IL-00119938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YISS ) YISSUM RES & DEV
                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arad G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-388042/33.
236
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234 LTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                              WO9829444-A1
                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaempfer R,
                                                                                                                                                              23-OCT-1998
                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                          AAW64647;
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62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC------AGGTPNKTACMYGGV 111

2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH

82; Conservative

Matches

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Local Similarity

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antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an anticancer immune response in vivo or ex vivo
                                                 172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor cell capable of stimulating antitumor immune reactivity in vitro or
in vivo comprises exogenous nucleic acids encoding a superantigen and a
                                                                                                                                               11
                                                                                  112 TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
-----AGGTPNKTACMYGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a tumour cell capable of stimulating
                                    PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-
                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus enterotoxin B protein
                                                                                                                                                                                                                                                                                                                                                                 Tumour; cancer; immune; enterotoxin
                                                                                                                                                                                                                                                                  AAB67341 standard; peptide; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 2, 16pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-00416530.
90US-00466577.
91WO-US000342.
92US-00891718.
93US-00025144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00491746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 costimulatory molecule
                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s.
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                                                                                                                                                                                 230 LYT 232
                                                                                                                                                                                                         LTT 236
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                                                                                                                                                                                                                                                                                                                                                                                                               US6180097-B1
                                                                                                                                                                                                                                                                                                                  23-APR-2001
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31-JAN-1994
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The present invention relates to novel peptides derived from Staphylococcus aureus enterotoxin B (SEB) protein. These peptides are capable of binding to immunoglobulin (19) E antibodies. However, unlike SEB, they do not induce proliferation of T cells. The peptides are useful as immunomodulators and inhibitors of cytokine production in T cells, particularly for treatment of atopic eczema, bronchial asthma, allergic sclerosis and for inducing or strengthening the Thi/Th2 immune responses, specifically for treating psoriasis, autoimmune uveitis, allergic contact eczema, Behcet's syndrome, diabetes mellitus, Hashimoto's thyroiditis,
                                                                   111
                                                                                                                                                          TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                               61
                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterotoxin B; SEB; immunomodulatory; IgE antibody; atopic eczema; lupus erythematosus; Crohn's disease; multiple sclerosis; psoriasis; rheumatoid arthritis; immunoglobulin B; dermatological; antiasthmatic; antiallergic; ophthalmological; antimogratic; antirheumatic; antiarthritic; neuroprotective; immunosuppressive; antinflammatory; vasotropic; antidiabetic; thyromimetic; antibacterial; gynaecological;
                                ESOPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDOFLYFDLIYSIKDTKL
EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                   PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV
                                                                                                     GNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGV
                                                                                                                                                                                                           SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide that binds immunoglobulin B and alters cytokine synthesis, useful for treating e.g. atopic eczema, asthma or allergy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified Staphylococcus aureus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 45-46; 46pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                      ABG75016 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis, useful for treating also its encoding nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002DE-01007734.
2002DE-01040866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2003; 2003WO-EP001511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGEL-) AGELAB PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-646480/61
                                                                                                                                                                                                                                                                                230 LYT 232
                                                                                                                                                                                                                                                                                                                  234 LTT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG75016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuber K;
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Gaps

19;

Length 239; Indels

ch 24.2%; Score 299.5; DB 4; Similarity 33.7%; Pred. No. 2.1e-21; 82; Conservative 46; Mismatches 96;

Best Local Similarity Matches 82; Conserv

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Schlievert PM, Roggiani M,
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                    RESULT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel modified proteins that exhibit the biological activity of Staphylococcal enterotoxin B (SEB) with reduced immunogenicity compared to wild type proteins having the same biological activity. Specifically, it refers to the identification of T-cell peptide
                                                                                                           ô
                                                                                                                                                                    111
                                                                                                                                                                                        118
                                                                                                                                                                                                           TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                              61
                                                                                                                                                58
  disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    staphylococcal
to evoke an
          multiple scierosis, organ transplant rejection, rheumatoid arthritis a spontaneous, recurrent abortion. They can also be used, in vitro, for inhibiting IFNgamma production and for modulating spontaneous or stimulated cytokine production in Th1/Th2 cells. Note: No further information about this sequence is given in the specification
                                                                                                                                               1 ESQPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL
                                                                                                                                                                               EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDOFLENTLLFKGFFTGH
                                                                                                                                                                     PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV
                                                                                                                                                                                                                                                    SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                           Gaps
                                                                                                           19;
  Helicobacter pylori, lupus erythematosus, Crohn's
                                                                                      Length 239;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New modified molecule having the biological activity of enterotoxin B (SEB), useful as determinants on SEB able
                                                                                                                                                                                                                                                                                                                                                                                                                         Wild type Staphylococcus aureus enterotoxin B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            staphylococcal enterotoxin B; SEB; immunogenicity;
                                                                                                           96;
                                                                                      Score 299.5; DB 7;
Pred. No. 2.1e-21;
                                                                                                           46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell peptide epitope; immune response.
                                                                                                                                                                                                                                                                                                                                                               protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-2003; 2003WO-EP009116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2002; 2002EP-00018229
                                                                                      24.2%;
larity 33.7%;
Conservative 40
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr FJ, Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-226855/21
                                                                                                                                                                                                                                                                                                                                                                ADL14247 standard;
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                            LYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004018684-A2.
                                                                      Sequence 239 AA
                                                                                                                                                                                                                                                                                                                LT
   infection by
                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-2004
                                                                                                            82;
                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                    ADL14247;
                                                                                                                                                                      62
                                                                                                                                                                                          5
                                                                                                                                                                                                                                                     172
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                              RESULT 75
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                        ADL14247
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                                                                                                                                                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                    61
epitopes derived from SEB that can be modified in order to create variants that are non-immunogenic. The present invention describes designing SEB analogues containing amino acid substitutions in the most immunogenic regions. Accordingly, the resulting modified molecules are useful as determinants on SEB able to evoke an immune response. This polypeptide sequence is the Staphylococcus aureus enterotoxin B protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                          1 ESQPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL
                                                                                                                                                                                                                                                                                                                                                                                                    SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                              PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                         Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neutralising antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild type Cys replaced by
                                                                                                                                                                                                                         ; Score 299.5; DB 8;
; Pred. No. 2.1e-21;
46; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stoehr J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .30
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW12153 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protection; treatment; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00480261
                                                                                                                                                                                                                           24.2%;
33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                     Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9640930-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                             Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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Mutant SPE-A toxin with at least one amino acid change is non-lethal - used in vaccine composition for treatment of streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Tyr substitued by Ala"

    aureus periplasmic enterotoxin B mutant Y94A.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27. .266
/label= Mature_SEB_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .26
|Tabel= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                ABU62455 standard; protein; 266 AA
                                                 Example 4; Page; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                             27-AUG-2003 (first entry)
                                                                                                                                                                                Local Similarity 34.2% nes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
      WPI; 1997-099936/09.
                                                                                                                                                              Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003036644-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                               ABU62455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to ceither the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, peptide, diagnosing superantigen toxin peptide, diagnosing superantigen toxin peptide, diagnosing superantigen toxin peptide, diagnosing superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an antiser a isolated from individuals immunised with one or more altered to treating/ameliorating a superantigen-associated bacterial infection, an antised and surpercoccal pyrogenic enterotoxin A, B, Cl (SEA, CT SSE). The superantigen toxin and an antibody which recognises altered TSST-CT superantigen toxin and an antibody which recognises altered TSST-CT SSEB, SECI) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA, CSEB, SECI) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA, CSEB, SECI) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA, CSEB, SECI) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence mutant of SEB. Note: The present sequence is not shown in the specification but was created by the indexer using the wild-type sequence of the information in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGG-----TPNKTACMYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.0%; Score 297.5; DB 7; Length 266; 33.2%; Pred. No. 3.8e-21; tive 44; Mismatches 100; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page; 68pp; English
                       26-NOV-2001; 2001US-00002784.
                                                                            97US-00882431.
98US-00144776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Conservative
                                                                                                                                                                                                                                                                              WPI; 2003-492125/46.
                                                                                                                                                                 (ULRI/) ULRICH R G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 YLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 YLTT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 266 AA;
                                                                                                         01-SEP-1998;
                                                                               25-JUN-1997;
                                                                                                                                                                                                                         Jlrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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8
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                                                                                                                                                                                                                                          The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SBE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           substantially cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 ETGYIKFIPKNKESFWFDFFPPFFTGSKY----LMIYKDNETLDSNTSQIEVYLIT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.0%; Score 297.5; DB 2; Length 251; 34.2%; Pred. No. 3.5e-21; tive 45; Mismatches 92; Indels 19
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AAR13209 standard; protein; 221 AA

RESULT 78

AAR13209

AAR13209 ID AAR1 XX AC AAR1 XX

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19-DEC-2000; 2000US-00741503
Staphylococcus aureus.
                                                                                                                                     rerman DS, Stone JL;
                                                                                                                                                        WPI; 1993-405418/50.
                                                                                                      (TERM/) TERMAN D S.
                                                                                                                STON/) STONE J L.
                                                                                                                                                                                                                                                                                                                    Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002051765-A1
                   WO9324136-A1.
                                                            01-JUN-1993;
                                                                                 01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2002
                                       09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB76240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 80
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGKQTIVPIDKVKTSKKEVIVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
                                                                                                                                                                                                                                                                                                         SPE A can be used for tumouricidal treatment, esp. with a haemolysin. Synthetic polypeptides having structural homology to Streptococcal pyrogenic exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VSGPNYDKLKTELK
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                           Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity Staphylococcal protein A without potential toxic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 221;
                                                   SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcal enterotoxin; SB; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 ESFWFDLFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 296.5; DB 2; Length 35.6%; Pred. No. 3.7e-21; ive 42; Mismatches 84; Indels
                              pyrogenic enterotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR45017 standard; protein; 221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcal enterotoxin SPE A.
                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 74pp; English
                                                                                                                                       90US-00466577
                                                                                                                                                           90US-00466577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative
  (revised)
                                                                                                                                                                                                                         WPI; 1991-237984/32.
                                                                                                                                                                               (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 221 AA;
                                 Streptococcal
                                                                         Streptococcus
                                                                                                                                       17-JAN-1990;
                                                                                                                                                           17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
08-JUN-1994
27-AUG-2003
15-OCT-1991
                                                                                            WO9110680-A.
                                                                                                                  25-JUL-1991
                                                                                                                                                                                                      Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR45017;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR45017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 SELQRNAL-SNIRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exotoxin A; SPE A; superantigen; antigen; tumour; cancer; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ESPWFDLFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVSYDLFD----AQGOYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.9%; Score 296.5; DB 2; 35.6%; Pred. No. 3.7e-21; iive 42; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus pyogenes exotoxin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1, 90pp, English
                                                           92US-00891718.
93WO-US005213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB76240 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 35.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal animals against which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the sepecification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYY---GYQCAGGTPNKTACMYGGVTLHDNN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLSYLCENA--ERSACIYGGVTNHEGN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLTEEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 KVQRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           substantially cancer and
Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYN---VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTG
              protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome, STSS; symptom; amelioration; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -A toxin with at least one amino acid change is - used in vaccine composition for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90; Indels
                                                                                                                                                                                                                                                               /note= "wild type Cys replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.9%; Score 296.5; DB 2 34.3%; Pred. No. 4.4e-21; iive 44; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stoehr J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   streptococcal toxic shock syndrome etc
                                                                                                                                                                         . .30
|abel= sig_peptide
                                                                                                                                                                                                        31. .251
/label= mat_peptide
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPE-A toxin with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sxample 4; Page; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                         95US-00480261.
                                                                                                                                                                                                                                                                                                                                                                       96WO-US010252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roggiani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-099936/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 251 AA;
                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlievert PM,
                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                      19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-lethal
                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                         Peptide
                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes. Similarity is shown, in several stretches of sequence, between staphylococcal enterotoxins, streptococcal pyrogenic sequence, between staphylococcal enterotoxins, streptococcal pyrogenic sequence, between staphylococcal exfoliative toxins (see ABB76234-44). In the present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive T and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B, and to streptococcal pyrogenic exotoxins, with statistically significant sequence homology and similarity (Z value of Lipman and Pearson algorithm in Monte Carlo similar hydropathy profiles. These superantigens are used to treat solid tumours, including their metastases, without radiation, surgery or standard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with one or more superantigens ex vivo to generate stimulated cells into the a specific V beta subset of cells, and reintracolucing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reagent for treating cancer without the need for e.g. radiotherapy, comprises a specific V beta subset of T cells sensitized to a growing tumor and stimulated with superantigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG
                                                                                                                                                                                                                                                                                                                                                                       present sequence is the protein sequence of exotoxin A (SPE A) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patient to induce an in vivo therapeutic, tumouricidal reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 296.5; DB 5; Length 221; 35.6%; Pred. No. 3.7e-21; ive 42; Mismatches 84; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STVSYDLFD----AQGOYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESFWFDLFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW12151 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23...
35.6%; FA.
                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 17pp; English.
            89US-00416530.
90US-00466577.
91WO-US000342.
92US-00891718.
94US-00189424.
95US-00491746.
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                                                                                                                                                                                                                            WPI; 2002-415198/44.
                                                                                                                                                       DS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 221 AA;
                                                                                                                                                       (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1997
                                                                                                                      19-JUN-1995;
                03-OCT-1989
17-JAN-1990
                                                                   01-JUN-1992
                                                 17-JAN-1991
                                                                                                    31-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
                                                                                                                                                                                           Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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XX AAW1
XX DT 04-N
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120 TEEKKVPINLMIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-011997/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 251 AA;
                                                                                                                                                                                                                                                                                                     WO2003094846-A2.
                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002;
28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2002;
                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Terman DS;
                                                                                                                                                                  ADF89839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                             protection, treatment, cancer, neutralising antibody, streptococcal toxic shock syndrome, STSS; symptom, amelioration, fever, hypotension, group A streptococcal infection, myositis, fascitis, liver damage, T cell; lymphoma; ovarian; uterine.
                                                                                                                    non-lethal; mutant; production; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 SQEVFAQQDPDPSQLHRSSLVNNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIXN---VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 251;
                                                                                            Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%; Score 295.5; DB 2; Length 2 34.2%; Pred. No. 5.6e-21; ive 46; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                     /note= "wild type Lys replaced by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlendorf
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stoehr J,
                                                                                                                                                                                                                                          1. .30
/label= sig_peptide
                                                                                                                                                                                                                                                                 31. .251
/label= mat_peptide
                                                                                                                                                                                                                               Location/Qualifiers
                      standard; protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page; 102pp; English.
                                                                                                                    Streptococcal; toxin A; SPE-A;
                                                                                                                                                                                                                                                                                                                                                                             96WO-US010252
                                                                                                                                                                                                                                                                                                                                                                                                     95US-00480261
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roggiani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34...
Best Local Similarity 34...
                                                                    (first entry)
                                                                                                                                                                                             Streptococcus pyogenes.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-099936/09.
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                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schlievert PM,
                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
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                                                                     04-NOV-1997
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                                              AAW12150;
                      AAW12150
                                                                                                                                                                                                                                         Peptide
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RESULT 82
            AAW1215(
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9
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                                                                                              180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                    4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superantigen; SAg; enterotoxin; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcal pyrogenic exotoxin A (SpEA) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%; Score 295.5; DB 8; 34.2%; Pred. No. 5.6e-21; withough 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 16; 91pp; English
                                                                                                                                                                                                                                                                                                                                   ADF89839 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyrogenic exotoxin; SpE; SpEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0389366P.
2002US-0406697P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2002; 2002US-0406750P
01-OCT-2002; 2002US-0415310P
02-OCT-2002; 2002US-0415400P
09-JAN-2003; 2002US-0415400P
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                HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                              120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                   GPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                   Streptococcal; toxin A; SPB-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis;
                                                                                                                                                               180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "wild type Ser replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlievert PM, Roggiani M, Stoehr J, Ohlendorf
                                                                                                                                                                                                                                                                                                                                                                                                                                                        liver damage; T cell; lymphoma; ovarian; uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 30
|abel= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/label= mat_peptide
                                                                                                                                                                                                                                                            AAW12154 standard; protein; 251 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
Synthetic.
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                                                82
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                                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                  120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                 The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
                                                                                                                                                         81
                                                                                 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcal; toxin A, SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substantially cancer and
                                                                                                                                                                                                                                                          180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYŢ 232
                                                                                                                                                                                                                                                                        : | | | :: | | :: | | ETGYIKFIPKNKESFWFDFFPEPETQAXY----LMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                   25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIXN---VS
                                                    Gaps
                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
                      Length 251;
               Score 294.5; DB 2; Lens...
Pred. No. 7.18-21;
Pred. No. 7.18-21; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant SPE-A toxin with at least one amino acid change is non-lethal - used in vaccine composition for treatment of streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "wild type Lys replaced by Glu"
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                                                      45; Mismatches
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/label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              AAW12146 standard; protein; 251
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                         23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                      81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes
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                         Query Match
Best Local Similarity
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Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlievert PM,
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                                                                                                                                                                                                                                                                                       198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                          Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                       61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                   120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                   toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms. e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A is be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                     82 GPNYDKLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL 141
                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                        25 SQEVFAQQDPDPSQLHRSSLVKNLQNİYPLYEGDPVTHENVKSVDQLLSHHLIYN---VS
against wild type SPE-A and to treat cancer and streptococcal
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             19;
                                                                                                                                                                                             Length 251;
                                                                                                                                                                                                                            92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlendorf D;
                                                                                                                                                                                               Score 294.5; DB 2;
Pred. No. 7.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes Streptococcal toxin A.
                                                                                                                                                                                                                             45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stoehr J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 30
/label= Big_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW12097 standard; protein; 251 AA
                                                                                                                                                                                                 23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US010252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00480261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                             Best Local Similarity 34.2
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MINU ) UNIV MINNESOTA
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N-PSDB; AAW12097.
                                                                                                                                                                    Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                                                                                                                                                                 Query Match
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                                                                                                   Streptococcus pyogenes Streptococcal toxin A (SPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TEEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -A), from which a non-lethal mutant SPE-A, compitaing at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to mentralising antibodies (Ab) to be produced, which may be used to infection, myositis, fascitis and liver damage. The neutralising A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 ETGYIKFIPKNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 QRGLIVPHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT
                                                                                                                                                                                                                                                                                                                                                                       23.8%; Score 294.5; DB 2; Length 251; 34.2%; Pred. No. 7.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp.
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                                                                                                                                                                                                                                                                                                                                                                                                          45; Mismatches
                                   streptococcal toxic shock syndrome etc.
                                                                  Disclosure; Page 77-79; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .30
label= sig_peptide
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                                                                                                       sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                    Sequence 251 AA;
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Matches
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31. .251
/label= mat_peptide
/label= sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-099936/09
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                                                          Misc-difference
                                                                                                                                                                                                                                          17-JUN-1996;
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                      Peptide
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                                                                                                                                                                                                                                                                                                                 The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A is especially useful toxic will specially useful toxic neutral special calls. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 EIPKKIVVKVSIDGIQ-SLSFD-IETNKKAVYTAQELDYKVRKYLTDNKQLYTNGF--SKY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 SQEVFAQQDPDPSQLHRSSLVKNLQDIYFLYEGDPVTHENVKSVDQLLSHHLIXN---VS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                   Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Indels
                                                                                                                      Ohlendorf D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; Score 294.5; DB 2; 34.2%; Pred. No. 7.1e-21; tive 45; Mismatches 92;
                                                                                                                      Stoehr J,
                                                                                                                                                                                                                                          streptococcal toxic shock syndrome etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW12148 standard; protein; 251
                                                                                                                                                                                                                                                                                  Claim 5; Page; 102pp; English
96WO-US010252
                                         95US-00480261
                                                                                                                      Schlievert PM, Roggiani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1997 (first entry)
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                                                                              (MINU ) UNIV MINNESOTA
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les 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 251 AA;
    07-JUN-1996;
                                         07-JUN-1995;
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Matches

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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin A (SPB-A) mutant, which can be used to produce vaccines to protect animals against wild type SPB-A and to treat cancer and streptococcal toxic shock syndrome (STS). The mutant SPB-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, amositie, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPB-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPB-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPB-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is a non-lethal Streptococcus pyogenes Streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | ::| | | ::| | STGYIKEIPKONKESFWFDFFPBPFFTQSXY----LMIYKONFTLDSNTSQIEVYLIT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 SQEVFAQQDFDPSQLHRSSLVKNLQDIYFLYEGDPVTHENVKSVDQLLSHHLIYN---VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SEEINEKDLRKKSELORNAL-SNLROIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 23.8%; Score 294.5; DB 2; Length 251; Local Similarity 34.2%; Pred. No. 7.1e-21; nes 81; Conservative 45; Mismatches 92; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of Streptococcus pyogenes exotoxin A.
                                                                     /note= "wild type Lys replaced by Glu"
'note= "wild type Asn replaced by Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlendorf D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stoehr J,
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81

Location/Qualifiers

Streptococcus pyogenes

THE KEY KAN THE STATE OF STATE

Synthetic

Key Peptide

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This is the amino acid sequence of the Streptococcus pyogenes exotoxin A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1 as change and is nonlethal compared with a protein to wild type SPE-A toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies that neutralise wild type SPE-A toxin activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. The used to protect against the development of streptococcal toxic shock syndrome (STSS). In addition, the toxins can be used for treating animals with symptoms of streptococcal infection nor STSS and in methods for stimulating T cell proliferation and in the treatment of cancer. In particular they can be used for treating T call lymphomas, and ovarian and uterine cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TEEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGLIVEHSSEGSTVSYDLFD----AQGOYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or treatment of streptococcal infection or toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 294.5; DB 2; Length 251; 34.2%; Pred. No. 7.1e-21; ive 45; Mismatches 92; Indels 19.
              SPE-A toxin, nonlethal; mutant; Streptococcus pyogenes exo
wild type; nontoxic; antibody; vaccine; immunity; ovarian
streptococcal toxic shock syndrome; STSS; T cell lymphoma;
                                                                                                                                                                                                                                                                                                      Ohlendorf D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcal group C enterotoxin SEC3-FR1909.
                                                                                                                                                                                                                                                                                                      Stoehr J;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06254 standard; protein; 239
                                                                                                                                                                                                  97WO-US022228
                                                                                                                                                                                                                                    96US-0032930P
                                                                                                                                                                                                                                                                                                      Schlievert PM, Roggiani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Conservative
                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                     (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                    WPI; 1998-333330/29.
N-PSDB; AAV41593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 251 AA;
                                                                  uterine cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-1999
                                                                                                                                                                                                    05-DEC-1997;
                                                                                                                                                                                                                                    06-DEC-1996;
                                                                                                                                 WO9824911-A2
                                                                                                                                                                   11-JUN-11998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 90
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ID AAY
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AC AAY
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DT 23-3
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This protein represents the Staphylococcus aureus type C enterotoxin SEC3-FR1909. The invention relates to pyrogenic toxins, such as staphylococcal enterotoxins, modified in the disulfide loop region. Typically, the modification involves deletions within the disulfide loop region of SEC (see AAv66261). The modified toxins retain useful biological properties, such as the ability to induce cytokine production, but have substantially reduced toxicity compared to the corresponding unmodified native toxin. Emetic response inducing activity and fever inducing activity are typically decreased by at least about 100-fold, while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| ::| | | | | | | | : | | : | | : | | : | | : | | ELINEDLANKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTSGKTCMYGGITKHEGNHFDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 DLRKKSELQRNALSNIRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DLHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVKT
             SEC3-FRI909; toxin; disulfide loop; protein engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified pyrogenic toxin, disulphide loop, fever-inducing activity, emetic response-inducing activity, staphylococcal enterotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.7%; Score 293.5; DB 2;
33.3%; Pred. No. 8.3e-21;
ive 48; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                           Non-toxic modified staphylococcal enterotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal enterotoxin SEC3-FR1909
                                                                     Location/Qualifiers 93. .110
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 17; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG71370 standard; protein; 240 AA
                                                                                                                                                                                             98WO-US025107.
                                                                                                                                                                                                                             97US-0067357P.
                                                                                                                                                                                                                                                             FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.33
Matches 78; Conservative
                                               Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                            WPI; 1999-358008/30.
                                                                                                                                                                                                                                                            (IDAH-) IDAHO RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 239 AA;
                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              native toxin
                  Enterotoxin;
                                                                                                                                                                                             11-DEC-1998;
                                                                                                                                                                                                                             02-DEC-1997;
                                                                                                                                                            10-JUN-1999
                                                                                                                                                                                                                                                                                              Bohach GI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
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Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
                                                                                                                                 JS6399332-B1
                                                                                                                                                                                                                       01-SEP-1998;
                                                                                                                                                                                                                                                               25-JUN-1997;
                                           attenuation
                                                                                                                                                                            04-JUN-2002
                                                                                                                                                                                                                                                                                                                                                     Ulrich RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU10083
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  $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a modified pyrogenic toxin derived from a native disulphide loop-containing pyrogenic toxin where the modified toxin comprises a disulphide loop having no more than 10 amino acids. The modified toxin has a fever-inducing activity or an emetic response-inducing activity decreased by about 100-fold in comparison to a native toxin. The modified pyrogenic toxin, that is a staphylococcal enterotoxin, is useful for non-specifically enhancing an immune function and for vaccination against diseases such as toxic shock syndrome and food poisoning. This sequence represents the staphylococcal enterotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified staphylococcal enterotoxin derived from a native disulfide loop-containing pyrogenic toxin, useful for non-specifically enhancing an immune function and as a vaccine against toxic shock syndrome or food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVKT
  toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGYIKFIESNGNTFWYDMMPAPGDKFDQSKYLMIYKDNKMVDSKSVKIEVHLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%; Score 293.5; DB 6; Length 240; 33.3%; Pred. No. 8.3e-21; ive 48; Mismatches 89; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                       Bohach CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcal enterotoxin B vaccine (B42360210).
                                                                                                                                                                                                                                                                                                                                                                                                                       Bohach GA,
                                                                                                                                                                                                                                                                                                                                                                                                                       Berger PH,
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 15, 67pp, English.
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                                                                                                                                                     /label= unknown
                                                                                                                                                                                                                                                                                      11-APR-2002; 2002WO-US011619
                                                                                                                                                                                                                                                                                                                                 13-APR-2001; 2001US-0283720P.
                                                                                                                                                                                                                                                                                                                                                                            (IDAH-) IDAHO RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Shiel PJ,
                                                                 aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-058608/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 78; Conserv
                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 240 AA;
                                                               Staphylococcus
                                                                                                                                                                                                WO200283169-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     Marshall MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-2002
                      SEC3-FRI909
                                                                                                                                                                                                                                           24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
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Matches
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8X4X4X8
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61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the protein sequence of staphylococcal enterotoxin B (SEB) vaccine B42360210. The invention relates to a vaccine against superantigen toxin-associated bacterial diseases. Superantigen vaccines were developed by engineering changes in the receptor-binding portions of superantigen toxins such as SEB to reduce receptor-binding affinities and toxicity while maintaining antigenicity. In examples from the invention, attenuated superantigen toxins were shown to protect animals against challenge with wild-type toxin. Methods of producing and using the altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided. A multivalent vaccine consisting of altered superantigen toxins SEC-1, TSST-1 and streptococcal SPEa is predicted to provide protective immunity against the majority of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%; Score 293.5; DB 5; 32.8%; Pred. No. 9.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 41-43; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bavari S;
                                                                                                                                                                                                               98US-00144776.
                                                                                                                                                                                                                                                                                 97US-00882431.
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                                                                                                                                                                                                                                                                                                                                                  (USSA ) US SEC OF ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                           Olson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-546281/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABN84224
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Claim 12; Page 23-24; 50pp; English.
             Staphylococcal enterotoxin B #1.
    (first entry)
                                                                                                                                                                                                                                                 80; Conservative
                                                                                                        Ulrich RG, Olson MA,
                                                                                                                 WPI; 2003-401542/38
                                                                                    (ULRI/) ULRICH R G.
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                         (OLSO/) OLSON M A. (BAVA/) BAVARI S.
                                                                                                                                                                                                                                                                                                                                                263
                                     Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                      YLYT 232
                                                                                                                     N-PSDB; ACA61179
                                                                                                                                                                                                                              Sequence 266 AA;
                                               US2003009015-A1
                                                                                                                                                                                                                                                                                                                                               YLTI
                                                                  25-JUN-1997;
                                                                           25-JUN-1997;
     11-AUG-2003
                                                        09-JAN-2003
                                                                                                                                             infection
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                                                                                                                                                                                                                                                                                                                                                260
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fragment is altered so that binding of the encoded altered toxin to either the MHC class II or I cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) infection, a vaccine (comprising an altered auperantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :| ||| |:: | 37 AESQPDPKPDELHKSSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIXDTK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered antisera isolated from individuals immunised with one or more altered 1. Also disclosed are mutated staphylococcal enterotoxin A, B, CI (SEA, SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SFBa and composition for treating or preventing bacterial infection. The presents sequence represents wild-type SEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated and purified superantigen toxin DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 19; Gaps
                                                                                                                                                                                                               SEB; staphylococcal enterotoxin B; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 293.5; DB 7; 32.8%; Pred. No. 9.7e-21;
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 aureus wild-type enterotoxin B, SEB.

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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                         ABU62326 standard; protein; 266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 28. .266
/label= Mature_SEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00882431.
                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
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N-PSDB; ACD28896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ULRI/) ULRICH R G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003036644-A1.
                                                                                                                                                                                                                                                               antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1997;
01-SEP-1998;
                                                                                                                             27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003.
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                                                                                  ABU62326;
                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                    ABU62326
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating particularly useful for producing vaccine against superantigen toxins, particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New superantigen toxin and/or DNA fragment with an altered binding of the encoded altered toxin to either MHC class II or T cell antigen receptor, useful for treating or ameliorating superantigen-associated bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                               Enterotoxin B; superantigen-associated bacterial infection; vaccine; superantigen toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bavari S;
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The present invention relates to a tumour cell capable of stimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an anticancer immune response in vivo or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor cell capable of stimulating antitumor immune reactivity in vitro or in vivo comprises exogenous nucleic acids encoding a superantigen and a costimulatory molecule.
                                                                                             259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 SKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                               SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VSGPNYDKLKTELK
                 16 SELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG
VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY
                                                              171 NSDSFGGKVORGLIVPHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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35.1%; Pred. No. 9.3e-21;
ive 42; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyrogenes toxin A protein.
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                                                                                                                                                                                                                                                  AAB67344 standard; peptide; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-00416530.
90US-00466577.
91WO-US000342.
92US-00891718.
94US-00189424.
95US-00491746.
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                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes
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                                                                                                                                 232
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                                                                                                                                                                                                                                                                                                                                                                                     cancer;
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                                                                                                                              229 YLYT
                                                                                                                                                             260 YLT
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02-MAR-1993
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                                                                                               202
--AGGTPNKTACMYGG 110
                                                               VILHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                 171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of waccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is a protein related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AESOPDPKPDELHKSSKF--TGLMEDMKVLYDDNHVSAINVKSIDOFLYFDLIYSIKDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG
                                                                                 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superantigen toxin; vaccine; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.7%; Score 293.5; DB 7;
llarity 32.8%; Pred. No. 9.7e-21;
Conservative 45; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 114-115; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein #3 related to the invention.
                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                  AAE37678 standard; protein; 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2001; 2001WO-US046540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-2001; 2001US-00002784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-492125/46.
N-PSDB; AAD56766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                 232
                                                                                                                                                                                                                                YLTT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003056015-A1
                                                                                                                                                                                               YLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                   36-OCT-2003
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                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                 AAE37678;
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treating cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ESQPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59. GNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                      172 SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and homologues - for auto-immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.6%; Score 292.5; DB 2; Best Local Similarity 34.0%; Pred. No. 1e-20; Matches 82; Conservative 44; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of staphylococcal enterotoxin(s) in a patient or for the treatment of
                                                                                                                                                                                                                      AAR45014 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1, 90pp, English
                                                                                                                                                                                                                                                                                                                                                         Staphylococcal enterotoxin SEB.
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                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Terman DS, Stone JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-405418/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STONE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TERMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 239 AA;
                                                                                L 230
                                                                                                                     L 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9324136-A1
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                                                                                                                                                                                                                                                                                                25-MAR-2003
08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1993.
                                                                                                                                                                                                                                                             AAR45014;
                                                                                                                     234
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(STON/)
                                                                                                                                                                               RESULT 98
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                                                                                                               요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                    DGIQ-SLSFD-IETNKKAVTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 TLHDNNRLTBEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                             DGKQTTVP1DKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEB. Synthetic polypeptides having structural homology to Staphylococal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was isolated and purified from S.aureus. It can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EKSEBINEKOLRKKSELORNALSNIROIYYYNEKAITENKESDDOFLENTLIFKGPFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ESQPDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity Staphylococcal protein A without potential toxic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.6%; Score 292.5; DB 2; Length 239; 34.0%; Pred. No. 1e-20;
                                                                                                                                                              : : | | : : | | : | | : | | : | | : | | ESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
                                                                                                                                         STVSYDLFD----AQGOYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                            tumouricide
                                                                                                                                                                                                                                                                               AAR13206 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEB; cancer treatment; pyrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-00466577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-00466577
                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 34.0
hes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-237984/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                            15-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9110680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUL-1991,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Terman DS;
                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                      AAR13206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                        64
                                                             132
                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHZ class II or Teall antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host call transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin, paptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an creating/ameliorating a superantigen-associated bacterial infection, an anissera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an entibody which recognises altered TSST-1 superantigen toxin and annibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, CI (SEA, SEB). SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and composition for treating or preventing bacterial infection. The present sequence represents the ESTQ (with reference to the mature protein
171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                          203 FFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKAVDSKDVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Glu substitued by Gln"
                                                                                                                                                                                                                                                                                                                                                                                            S. aureus periplasmic enterotoxin B mutant E670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Mature_SEB_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .26
label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                           ABU62453 standard; protein; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00882431.
98US-00144776.
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ULRI/) ULRICH R G.
                                                                                                                                      263
                                                                                          229 YLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003036644-A1
                                                                                                                                      260 YLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1997;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                 27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ulrich RG;
                                                                                                                                                                                                                                                                                                      ABU62453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                   ABU62453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A pair of nucleic acids comprising a portion of a long intergenic region (LIR) of a geminivirus genome lacking a sequence encoding a geminiviral coat protein, and a nucleic acid comprising a geminiviral replicase gene linked to a fruit ripening-dependent promoter, are new. Strains of Escherichia coli and Agrobacterium tumefaciens transfected with an expression vector containing the nucleic acids and a gene of interest auseful for the production of transgenic plants (or cells). The sequences and methods are useful for amplifying a gene of interest and overproducing a protein of interest in recombinant plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 LGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 144
177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMNYNDNKMVDSKDVKIEVY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids comprising a portion of a long intergenic region of a geminivirus genome and a sequence comprising a geminiviral replicase gene, useful for amplifying a gene of interest and overproducing a
                                                                                                                                                                                                                                                                                                                                                                                               Rep; replicase, rescue, replication, vector; gene expression, recombinant protein production; plant; intronless; enterotoxin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.6%; Score 292.5; DB 3; Length 266; 33.2%; Pred. No. 1.2e-20; tive 47; Mismatches 97; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hefferon KL, Arntzen C;
                                                                                                                                                                                                                                                                                                                                                 Plant-optimized mutant staphylococcal enterotoxin B.
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                                                                                                                                                                                                           AAY92319 standard; protein; 266 AA.
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Synthetic.
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                                             230 L 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-2000
                                                                                                                                                                                                                                                        AAY92319;
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Matches
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sequence) mutant of SEB. Note: The present sequence is not shown in the specification but was created by the indexer using the wild-type sequence and the information in the specification
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A);
266
Sequence

	7,	09	84
	Gaps	KGFFTG	SIKDİK
266;	19;	ENTLLE	YFDLIN
Length	Indels	KESDDOFI	VKSIDQFL
DB 7;	101;	SKAITEN	HVSAIN
23.5%; Score 291.5; DB 7; Length 266;	debt bocar Similatily 32.0%; ried. No. 1.55-20; fatches 80; Conservative 44; Mismatches 101; Indels 19; Gaps 7;	1 SEKSEEINEKDLRKKSELQRNALSNILRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60	27 AESQPDPKPDELHKSSKFTGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
23.5%;	ative 4	DLRKKSELO	ELHKSSKF-
tch	Matches 80; Conservat	1 SEKSEEINER	27 AESQPDPKPI
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	27 AESQPOPKPDELHKSSKFTGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84	61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGG 110	
-	ESQPDPKPDELHKS	PWYNDLLVDLGSKD	
••	27 A	61 HI	

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⁸⁵ LGDYDNVRVQFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 144

VTLHDNNRLTEBKKVPINLMIDGKQTTVPIDKVKTSKKBVTVQELDLQARHYLHGKFGLY 170 111

¹⁷¹ NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHJDL 228

²⁰³ EFNN--SPYETGYIKFIENENS-FWYDWAPAPGDKFAQSKYLAMYNDNKAVDSKDVKIEV 259

²²⁹ YLYT 232

²⁶⁰ YLT 263

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exotoxin 14 [impor cell shape deterni transferrin-bindin hypothetical prote	exotoxin 6 limport multidrug resistan trse-like protein	B. subtilis YjbK p flagellar hook pro flagellar hook pro	hypothetical prote phospholipase A2-1	DNA-directed DNA p hypothetical prote	hypothetical prote MG032 homolog B01	beta-fructofuranos arginyl tRNA synth	protein with Dnad	cell wall-associat	major blood-stage	glycosidase homolo	arginyl tRNA synth	hypothetical prote diphosphate-fructo	lactocepin (BC 3.4 MG288 homolog P02_	ABC transporter, A	exytanceyte memora exotoxin 15 [impor	transposase of 151 glycerol kinase -	chitinase chi-A or penicillin-binding	penicillin binding	penicillin-binding major surface glyc	hypothetical prote GAG protein - yeas	L1 protein - human ABC transporter, A	outer membrane ush	transposase of 151 hypothetical prote	hypothetical prote probable transcrip	hypothetical prote	transferin-bindin hypothetical prote	hypothetical prote	exotoxin 9 (import	rare lipoprotein A n-aminobenzoate sv	hypothetical secre	membrane conserved	probable ferric si	hypothetical prote upiquitin-like pro	hypothetical prote	tyrocidine synthet	exotoxin 8 [import replication protein	hypothetical prote	n F53H1.4 (etical prot	
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s igen Ltd.		15 Seconds ignments)	of million cell updates/sec	RDNKTINSENLHIDLYLYTT 233				: 283416					-			chance to have a	result being printe	•.		Dearrintion		enterotoxin A pre	enterotoxin P [im enterotoxin D pre	enterotoxin SeN	enterotoxin seo (extracellular ent	extracellular ent enterotoxin SEM [enterotoxin B pre	exotoxin type A p enterotoxin C3 -	enterotoxin C-2 p	exotoxin A precur exotoxin type A p	exotoxin type A p	enterotoxin C-1 p extracellular ent	streptococcal pyro	enterotoxin YENT2	exotoxin C precur hypothetical prot	enterotoxin Yentl	exocoxin is timpo toxic shock syndr	toxic shock syndro exotoxin 12 [impor	11 [i
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen	n search, using sw model	756, 2005, 11:00:34; Search time (without al		KKSELOR		Gapop 10.0 , Gapext 0.5	116 seqs, 96216763 residues	satisfying chosen parameters	h: 0	20000000	Minimum Match 0% Maximum Match 100%	sting first 200 summaries	79:*	pirs:*	pir3:* pir4:*	or of results predi	tesure predi		SUMMARIES	רד פר ליביים לי		257 2	260 2	258 2	242 2	240 2 .	266 1	251 1 266 2	266 2	236 2	236 2	266 1 258 2	250 1	136	235 2	133 2	232 2	234 2 B8 232 2 E8	231 2 D89
ບັ	OM protein - protein	Run on: July	Title: US-0	ct score: 12	older		Searched: 283416	Total number of hits	Minimum DB seq length:		Post-processing: Mir	Lii	Ħ.		3. t.	to: ON pose	φ.	and is derived	e e	Result Query	2000	1023	994	461.5	339.5	337	300.5	295.5	281.5	279.5	272.5	2566.5	245	197	183.5	123	107.5	27 105.5 8.5 28 101 8.2	99.5

176 77.5 6.3 361 2 B86692 N-acetylmuramoyl-L 177 77.5 6.3 372 2 G96933 HD-GYP bydrolase d thymidine phosphor 178 77.5 6.3 419 1 C53312 HD-GYP bydrolase d thymidine phosphor 178 6.3 457 2 G98933 Hyperelin, 47K type endo-1,4-beta-xyla G198 77.5 6.3 522 2 D96913 transferrin-bindin l81 77.5 6.3 547 2 S49815 transferrin-bindin hemolysin accessor 184 77.5 6.3 581 2 T51580 ovule development oligoment oligoment oligoment oligoment l82 77.5 6.3 590 2 H70130 oligoment oligoment oligoment l87 77.5 6.3 590 2 H70130 oligoment oligoment l87 77.5 6.3 609 2 T32302 sitce-specific reco sitce-specific reco 187 77.5 6.3 707 2 S78538 sitch-tical prote 187 77.5 6.3 707 2 S78538 sitch-tical prote 188 77.5 6.3 709 2 A41976 ribonuclease [impo proteinase related 190 77.5 6.3 1269 2 A90267	77.5 6.3 1325 1 S73723 77.5 6.3 3206 1 GNVSPV 77 6.2 425 2 T43772 77 6.2 620 2 E90575 77 6.2 646 2 H95155 77 6.2 646 2 H95155 77 6.2 876 2 S89344 77 6.2 893 2 S64926	ALIGNMENTS	RESULT 1 A28179 A28179 enterotoxin E precursor - Staphylococcus aureus C;Specise: Staphylococcus aureus C;Specise: Staphylococcus aureus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004 C;Accession: A28179 R;Cooch, J.L.; Soltis, M.T.; Betley, M.J.	A,Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene. A,Reference number: A28179; MUID:88257005; PMID:3384800 A,Accession: A28179 A,Molecule type: DNA A,Residues: 1-257 <cou> A,COSS-references: UNIPROT:P12993; GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002 C,Superfamily: enterotoxin B</cou>	Query Matc Best Local Matches 2		181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT 233
hypothetical prote cyclic beta 1-2 gl hypothetical prote probable carboxyl-DNA-directed RNA p alpha-amylase (EC beta-fructofuranos diphosphate-fructo hypothetical prote collagenase - Clos hypothetical prote surface antigen sp DNA helicase II BR metalloproteinase	serine/threonine-s transposase (06) B hypothetical prote hypothetical prote type II restrictio integrin alpha-1 c restin - human hypothetical prote hypothetical prote porin - common ice	hypothetical prote chromosome-associa chromodomain helic lactocepin (EC 3.4	hypothetical prote copper ABC transpo protection protection protection protection protection alpha-amylase - Th El protein - human DNA topolosmerase DNA topolosmerase DNA topolosmerase	microtubule-vesical hypothetical prote hypothetical prote uncharacterized co probable porin VC1 chorismate synthas transcription term transcription term	cystatulnine Deta hypothetical prote transferrin-bindin conserved hypothet hypothetical prote alpha-amylase (EC hypothetical prote	Lactocepin (EC 3.4 coagulation factor hypothetical prote probable lipopolys conserved hypothet hypothetical prote hypothetical prote probable secreted outer-membrane fim	hemolysin - Escher B. subtilis YvlB p p60-like (mycoplas glycosyl hydrolase hypothetical prote acctyl-CoA synthet hypothetical prote outer membrane sec glycosidase homolo probable membrane hypothetical prote hypothetical prote
103 81.5 6.6 1883 2 G82875 104 81.5 6.6 2870 2 H96974 105 81 6.5 299 2 AFI193 106 81 6.5 299 2 AFI193 107 81 6.5 299 2 AFI193 108 6.5 498 2 S93207 109 81 6.5 528 2 S93207 110 81 6.5 562 2 S9330 111 81 6.5 616 2 A36094 112 81 6.5 1021 2 140805 114 81 6.5 127 2 T21403 115 81 6.5 127 2 T21403 116 81 6.5 214 2 A97942	81 6.5 2485 1 80.5 6.5 361 2 80.5 6.5 413 2 80.5 6.5 413 2 80.5 6.5 1151 2 80.5 6.5 1427 2 80.5 6.5 1427 2 80.5 6.5 1427 2 80.5 6.5 1520 2 80.6 6.5 1520 2 80.6 6.5 1520 2	80 6.5 1008 2 80 6.5 1231 2 80 6.5 1388 2 80 6.5 1902 2	79.5 6.4 156 2 79.5 6.4 384 2 79.5 6.4 388 2 79.5 6.4 358 2 79.5 6.4 358 2 79.5 6.4 358 2 79.5 6.4 556 2 79.5 6.4 637 2	79.5 6.4 1321 2 79.5 6.4 2269 2 79.5 6.4 2894 2 79 6.4 348 2 79 6.4 378 2 79 6.4 378 2	7.9 6.4 620 2 7.9 6.4 660 2 7.9 6.4 660 2 7.9 6.4 108 2 7.9 6.4 1104 2 7.9 6.4 1131 2	79 6.4 2183 2 79 6.4 4981 2 79 6.4 4981 2 78.5 6.3 318 2 78.5 6.3 722 2 78.5 6.3 78.	78.5 6.3 998 2 78 6.3 416 2 78 6.3 476 2 78 6.3 669 2 78 6.3 669 2 78 6.3 691 2 78 6.3 993 2 78 6.3 1091 2 77.5 6.3 241 2 77.5 6.3 241 2 77.5 6.3 252 2

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C;Species: Staphylococcus aureus
C;Species: Obate: 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accesion: H9966
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I. C.; Shiba, T.; Hatcuri, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
Jancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Residues: 1-258 «KUR»
A;Cross-references: UNIPROT:Q9EZM4; GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P20723; GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758691
C;Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A33953
R;Bayles, K.W; I andolo, J.J.
Bacteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin lA;Reference number: A33953; MUID:89359112; PMID:2549000
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EEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                 148 EEKKVPINLWIDGKQNTVPLGTVKTNKKEVTVQELDLQSRHYLHETYNLYNTDAFNGKIQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                              enterotoxin D precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 NENIDSVKEKELHKKSELSSTALNNWKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTD
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                                                                                                                                                                                           181 RGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYTT
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Pred. No. 1.2e-46;
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Matches 126; Conservative
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A;Experimental source: strain N315
C;Genetics:
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-257 <BETS.
A; Cross-rences: UNIPROT: P13163; GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
A; Experimental source: strain FR1337
B; Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
B; Biol. Chem. 262, 7006-7013, 1987
A; Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A; Reference number: A29566; MUID:87222293; PMID:3584106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: C89984
R;Kurcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kurcda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 HSWYNDLLVDPDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTD
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             Betley, M.J.; Mekalanos, J.J.
Bacteriol. 170, 34-41, 1988
Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
Reference number: A28664; MUID:88086892; PMID:3335483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.6%; Score 1023; DB 2;
82.0%; Pred. No. 5.9e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 5.96
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 25-241,'S',243-257 <HUA>
C,Genetics:
A,Gene: entA
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Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 191; Conservative
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C;Superfamily: enterotoxin B
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A,Molecule type: DNA
A,Residues: 1-260 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                      A; Accession: A28664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: C89984
                                                                                                                                                                                                                                                                                                                                                                A;Accession: A29566
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; J. C.; Shiba, T.; Hatrori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: C99969
A;Accession: C99969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 < kURP.
A;Access-references: UNIPROT:085383; GB:BA000018; PID:gl3701621; PIDN:BAB42914.1; GSPDB:GN
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89991
B;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.; Lancet, S.; Aniba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-240 «KUR»
A;Cross-references: UNIPROT:09F0L7; GB:BA000018; PID:g13701803; PIDN:BAB43096.1; GSPDB:GA
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 YKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 KFKGKKLDIFGIDYNGPC-----KSKYMYGGATL-SGQYLNSARKIPINLWVNGKHKTI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK------VQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 LKGKNVDVFGISYKY----GSNSRT--IYGGVTKAENNKLDSPRIIPINLIINGKHQTVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 IDKVKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 VGNLRNFYTKHDYIDLKGVTDKNLPIANQLE-----FSTG---TNDLISESNNWDEIS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 27.4%; Score 339.5; DB 2; Length Stocal Similarity 35.6%; Pred. No. 2.5e-20; Local Sipervative 36; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 HSSEGSTVSYDLFDAQGOYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 337; DB 2; 35.3%; Pred. No. 3.9e-20;
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C;Superfamily: enterotoxin B
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A;Molecule type: DNA
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R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguo
R;Kuroda, M; Ohta, T; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K;
C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                           9
                                                                                                                                                                                                                                            88 VLKTSSLKVEFNSSDLANQFKGKNIDIYGLYFGNKCVGLTEEKTSCLYGGVTIHDGNQLD 147
                                                                                                                                                                                                                                                                                                                       121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                    85 ---NWLDGISAEPKDLKVEFSSSAISKEFLGKTVDIYGVYYKAHCHGEHQVDTACTYGGV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 SDSFGGKVORGLIVFHSSEGSTVS--YDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 - DRMISDVQKGYIKPHSHSEHKESFYYDLFYIKGNLPDQYLQIYNDNKTIDSSDYHIDVY 257
                                                                                                                                                                                                         61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 TGHPW-----YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                              32 EVDKKDLKKKSDLDSSKLFNLTS--YYTD--ITWQLDESNKISTDQLLNNTIILKNIDIS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 NEKD-----LRKKSELQRNALSNLRQIYYYNE----KAITENKESDDQFLENTLLFKGFF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 NEEDPKIESLCKKSSVDPIALHNINDDYINNRFTTVKSIVSTTE---KFLDFDLFKSI- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                               6 EINEKDLRKKSELQRNALSNLRQIYYYNEKAIT----ENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RGLIVFHS--SEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.3%; Score 387.5; DB 2; Length 260; Best Local Similarity 39.9%; Pred. No. 3.3e-24; Matches 97; Conservative 31; Mismatches 86; Indels 29
           | Similarity 41.2%; Pred. No. 3.1e-30; 96; Conservative 45; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: enterotoxin B
           Best Local Similarity
Matches 96; Conserv
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A; Residues: 1-260 < KUR>
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258 LFT 260
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A, Contenues: aumocation; Chymotryptic peptides
R;Huang, I.Y.; Bergdoll, M.S.
G. Biol. Chem. 245, 3439-3510, 1970
A,Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition A,Reference number: A92053; MUID:171007900; PMID:5470819
A,Contents: annotation; tryptic peptides
R;Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
B;Schantz, H. 1011-1016, 1965
A,Title: Purification of staphylococcal enterotoxin B.
A,Reference number: A90648; MUID:66035792; PMID:4953912
A;Contents: annotation; biological source of protein
R;Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni)
Bur. J. Biochem. 209, 823-828, 1992
A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B.
A,Reference number: S27240; MUID:93049338; PMID:1425690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N;Alternate names: erythrogenic toxin; scarlet fever toxin
C;Species: Streptococcus pyogenes phage T12
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 10-Sep-1999
C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R;Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) ge A;Reference number: S29659; MUID:86166804; PMID:3514452
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A;Molecule type: DNA
A;Residues: 1-251 - 4WES-
A;Residues: 1-251 - 4WES-
A;Cross-references: GB-140453; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1; PID:g1877430
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encoda A;Reference number: S18782; MUID:92044323; PMID:1940804
R;Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A;Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositic
A;Réference number: A92064; MUID:71007901; PMID:5470820
A;Contents: annotation; chymotryptic peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 BPNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMMYNDNKAVDSKDVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: protein

A; Residues: 28-42; 128-148

C; Superfamily: enterotoxin B

C; Keywords: enterotoxin; extracellular protein; toxin

C; Keywords: enterotoxin; extracellular protein; toxin

F; 127/Domain: signal sequence #status predicted <SIG>

F; 128-266/Product: enterotoxin B #status experimental <MAT>

F; 120-140/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 24.3%; Score 300.5; DB 1 Local Similarity 33.6%; Pred. No. 4.2e-17; hes 82; Conservative 47; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 YLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 YLTT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S27240
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Best Local S:
Matches 82,
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                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: D89969
A;Status: preliminary
A;Molecule type: DNA
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A; Reasdaces: 1-266 <-JON>
A; Reasdaces: 1-266 <-JON>
A; Cross-references: UNIPROT: P01552; EMBL: M11118; NID: g152999; PIDN: AAA88550.1; PID: g1530
A; Experimental source: strain S6
R; Huang, I.Y.; Bergdoll, M.S.
Biol. Chem. 245, 3518-3525, 1970
A; Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromid A; Reference number: A92065; MUID: 71007902; PMID: 5470821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q99T47; GB:BA000018; PID:g13701622; PIDN:BAB42915.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
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A;Molecule type: protein
A;Resicules: 28-55, NND', 59-68,'NE',71,'FDLIYL',78-117,119-127,'N',129,'D',131-132,'ENT'
A;Experimental source: strain S-6
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: S27366; A92065; S27240; A01815
R;Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A,Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A;Reference number: S27360; MuID:86168029; PMID:3957869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVPINLWIDGKQTTVPIDK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 HAVDVYGLSYSGYCL----KNKYIYGGVTL-AGDYLEKSRRIPINLWVNGEHQTISTDK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 VKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFHSSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKSVSTDKKMVTAQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSSKFYSGFDKGSVVFH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 NLRN--YYGSYPIEDHQSINPENNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLRQIYYYNEKAITENK -- ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
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                                                                                                                                                                                                                                                                                                       enterotoxin SEM [imported] - Staphylococcus aureus (strain N315)
                                                                                                           195 MNDGSNFSYDLFYTGYGLPESFLKIYKDNKTVDSTQFHLDV 235
                                                                         SSEGSTVSYDLFDAQGOYPDTLLRIYRDNKTINSENLHIDL 228
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|GSSFSYDLFDTGTGQAESFLKIYNDNKTVETEKFHLDV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 320; DB 2;
Pred. No. 9.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Mismatches
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33.0%;
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Best Local Similarity 33.04
Matches 72; Conservative
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          135
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A;Molecule type: protein
A;Residues: 28-66 <BHI2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 111, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the
A;Reference number: A33866; MUID:89327174; PMID:2473979
                                                                                                                                                                                                                                                                                                                                                                                             gene: sequence comparit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxin C-2 precursor - Staphylococcus aureus
NiAlternate names: enterotoxin C-3 precursor
C;Species Staphylococcus aureus
C;Species Staphylococcus aureus
C;Date: 10-Nov-1992 #sequence revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60114; B60114; Ā33866
C;Accession: A60114; B60114; Ā33866
C;Accession: A60114; B60114; Ā3386
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A;Reference number: A60114; MUID:89277549; PMID:2543637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-266 <HOV>
A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                     C.Species: Staphylococcus aureus
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Datession: S.11885
R.Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Genet. 220, 329-333, 1990
A.Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: seq
A.Reference number: S11885; MUID:90220508; PMID:2325627
ETGYIKFIPKNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 DLHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYDKVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.1%; Score 285.5; DB 2; Length Best Local Similarity 32.1%; Pred. No. 7e-16; Matches 75; Conservative 49; Mismatches 91; Indels
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A;Status: not compared with conceptual translation
                                                                                                                                                                                       enterotoxin C3 - Staphylococcus aureus
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A,Residues: 1-26c ABOH>
A,Cross-references: UNIPROT:P34071
A,Accession: B60114
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A; Residues: 1-266 <COU>
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C;Superfamily:
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A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassig
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X61556; NID:947291; PIDN:CAA43754.1; PID:947292
A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigne
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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                                                                                                          A;Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA41758.1; PID:g47288
A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X61555; NID:947309; PIDN:CAA43753.1; PID:947310
A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X61557; NID:947319; PIDN:CAA43755.1; PID:947320; Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned i
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Residues: 9-244 <NEH>
          nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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34.2%; Pred. No. 9.9e-17;
ative 45; Mismatches 92;
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Best Local Similarity 34.2
Matches 81; Conservative
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A; Residues: 9-244 <NEL>
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Residues: 9-228 <NES>
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exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isola NiAlternate names: scarlet fever toxin C; Species: Streptococcus pyogenes phage A; Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Vugoslavia; strain MGAS158 isolate Nebraska; strain MGAS485 isolate Vugoslavia; strain MGF C; Date: 29-24n-1993 #sequence revision 29-24n-1993 #text_change 16-Jul-1999 C; Accession: S18783; S18794; S18801; S18798 #text_change 16-Jul-1999 R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. J. Z71-1274, 1991 A;Title: Characterization and clonal distribution of four alleles of the speA gene encodi A;Reference number: S18782; MUID:92044323; PMID:1940804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA
A, Residues: 1-236 < AREA
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A, Residues: 1-236 < AREA
A, Residues: 1-236 < AREA
A, Residues: 1-236 < AREA
A, Residues: Strain MGAS485 isolate Yugoslavia unassigned phage
A, Note: the mucleotide sequence was submitted to the EMBL Data Library, September 1991
A, Accession: S18794
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-236 < AREA
A, Residues: 1-236 < AREA
A, Residues: 1-236 < AREA
A, Residues: 1-236 < AREA
A, Residues: SmBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
A, Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A, Rocession: S18801
A, Recession: S18801
A, Recession: Care and sequence not shown; translation not shown
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A; Residues: 1-236 <NEY>
A; Residues: 1-236 <NEY>
A; Residues: 1-236 <NEY>
A; Croser-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A; Croser-references: Extrain MGASC24 isolate Germany unassigned phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18798
A; Accession: S18798
A; Accession: S18798
A; Residues: nucleic acid sequence not shown; translation not shown
A; Residues: 1-236 <NEO>
A; Residues: 1-236 <NEO>
A; Residues: 1-236 <NEO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA
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33.3%; Pred. No. 2.7e-15;
w.omatches 91; Indels
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nes 77; Conservative 44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor N.Alternate names: scarlet fever toxin C.Species: Streptococcus pyogenes A.Variety: strain MGAS262 isolate California A.Variety: strain MGAS262 isolate California C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004 C.Accession: S18789
R.Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A,Title: Characterization and clonal distribution of four alleles of the speA gene encod A;Reference number: S18782; MUID:92044323; PMID:1940804
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFNS--SPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 GLNYDKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCRNAKRRACIYGGVTNHEGNHL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                            :| : | | | | : | : | : | | | : | : | 27 AESQPDFTPDELHKSSEF-TGTWGNMK--YLYDDHYVSATKVMSVDKFLAHDLIYNISDK
                                                                                                                                                                                                                                                                                                                                                                                        GHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVŢ
                                                                                                                                                                                                                                1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFPT
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                                                                                                                                                        19;
                                                                        Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2/Domain: signal sequence (fragment) #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-236 <NEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | | : | : | | | ETGYIKPISKOKETEMFOFPEPEFNQVKYLMIYKONETLDSSTSQI
                                                                                                                                                        Indels
7;28-266/Product: enterotoxin C-2 #status predicted <MAT>
                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 279.5; DB 2
Pred. No. 1.8e-15;
                                                                        22.7%; Score 281.5; DB 2 ilarity 31.1%; Pred. No. 1.5e-15; Conservative 50; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%;
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Best Local Similarity 33.5
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: enterotoxin B
Keywords: exotoxin
                                                                            Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLYT 232
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190 ETGYIKFIPKNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQI

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73

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A; Molecule type: DNA
A; Residues: 1.266 < BOH>
A; Cross-references: UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
A; Schmidt, J.J.; Sparo, L.
J. Biol. Chem. 258, 6300-6306, 1983
A; Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A; Reference number: A01816; MUID:8313327; PMID:6189824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: 806356; Aults F.M.
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nuclectide sequence of the staphylococcal enterotoxin Cl gene and relatedness (A;Reference number: 806356; MUID:88038352; PMID:2823067
A;Accession: 806356
                                                                                                                                                                                                                                                                                                                                                61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                            74 GPNYDKLKTELKKOGMATLFKDKNVDIYSVEYYHLCYLCENAERSACIYGGVTNHEGNHL 133
                                                                                                                                                                                                                                                                                                             120 TEEKKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                          4 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
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19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
21.5%; Score 266.5; DB 1; Length
Best Local Similarity 30.5%; Pred. No. 2.5e-14;
Matches 74; Conservative 51; Mismatches 101; Indels
92; Indels
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F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental
F;120-137/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin C-1 precursor - Staphylococcus aureus
43; Mismatches
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A,Residues: 28-75,'IL',78-176,'N',178-266 <SCH>
   77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: entCl
C,Superfamily: enterotoxin B
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   Matches
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                                                                                                                                                                           C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain isolate United Kingdom; strain MGAS496 isolate Germany
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1999
C;Accession: S18786; S18787; S18789; S18795; S18795; S18799
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod A;Reference number: S18786; MUID:92044323; PMID:1940804
                                                                                                                              exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol
N;Alternate names: scarlet fever toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-236 «NEA»

;Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760:1; PID:g47300

;Experimental source: strain MGAS251 isolate California unassignd phage

;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

;Accession: S18788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1.236 <NEZ>
;Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
;Cross-references: Expain MGAS256 isolate California unassigned phage
;Nete: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
;Accession: S18790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298; Experimental source: strain MGAS250 isolate California unassigned phage Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991; Accession: S18787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-236 <NEY>. Crossereferences: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306. Experimental source: strain MGAS285 isolate Colorado unassigned phage Experimental source: strain MGAS285 isolate Colorado unassigned phage inotes the nucleotide sequence was submitted to the EMBL Data Library, September 1991.
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Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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Gross-references: BMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318

'Bxperimental source: strain MGAS492 isolate United Kingdom unassigned phage

NOCE: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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"Cross-references: EMBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
"Experimental source: strain MGAS496 isolate Germany unassigned phage
"Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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Pred. No. 6.9e-15;
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33.3%;
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Best Local Similarity
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hypotherical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; S.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: A89942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 < kUR>
A;Kesidues: 1-157 < kUR>
A;Cross-references: UNIPROT: Q997P7; GB:BA000018; PID:g13701400; PIDN:BAB42694.1; GSPDB:GP
A;Experimental source: strain N315
C;Genetics:
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A;Bxperimental source: strain N315
C;Genetics:
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                                                                                                                                                                                                                                  A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: A89969 A;Status: preliminary
LGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEBKKVPINL 129
                                                 92 LKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKV 151
                                                                                                                                                                            130 WIDGKOT-TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHS 188
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C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C.Accesion: A89969
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                                                                                                                                                                                                                                                                                                                                                                                                         206 KNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 249
                                                                                                                                                                                                                                                                                                                                                        189 SEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
15.9%; Score 197; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 4.8e-09;
Matches 46; Conservative 28; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157;
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A; Residues: 1-136 < KUR>
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A;Gene:-yent2
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Matches
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NyAlternate names: scarlet fever toxin; SPE type A (speA)
NyAlternate names: scarlet fever toxin; SPE type A (speA)
Systems Streptococcus sp.
C;Species Streptoscoccus sp.
C;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta A;Reference number: A26152; MUID:86284313; PMID:3526093
                                                                                                                                                                                                           C;Accession..., G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutanl-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shina, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Gross-references: UNIPROT:085382; GB:BA000018; PID:913701617; PIDN:BAB42910.1; GSPDB:d
A.Experimental source: strain N315
                                                                                          extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N3
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLLVDLGSKDATNKYKGKKVDLYGAYYGYQCA------GGTPNKTACMYGGVTL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 255.5; DB 2
Pred. No. 1.9e-13;
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A.Rolecule type: DNA
A.Residues: 1-250 <JOH>
A.Cross-references: UNIPROT: P08095
C.Superfamily: enterotoxin B
C.Superfamily: enterotoxin B
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ilarity 29.1%;
Conservative 4
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C,Superfamily: enterotoxin B
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Best Local Similarity
.....hes 71; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-258 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 YLYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A26152
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c...o.c. staphylococcus aureus (strain N315)
C.Species: Staphylococcus aureus
C.Species: Staphylococcus aureus
C.Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C.Accession: F89807
M. A., M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch M.; M.; Ohta, T.; Uchiyama, I.; Baba, T.; Tinoue, R.; Katco, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                       enterotoxin Yentl [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89969
B;Muroda, M.; Ohtes, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizuteni-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, K.; Lance, 357, 1225-1240, 2001
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A;Molecule type: DNA
A;Rosaidues: 1-222 **KORS-
A;Crosa-references: UNIPROT:Q99WH4; GB:BA000018; PID:g13700319; PIDN:BAB41617.1; GSPDB:G?
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIRROT:099148; GB:BA000018; PID:gl3701620; PIDN:BAB42913.1; GSPDB:GRA;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 ---KILKTERNNKSLSDKYKNKOVDLFGTNYYNQC-----YFSL---DNMELND 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LFKGFFTGHPWYNDL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A,Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 KPEQLN-----KASEF-TGLMDNMR--YLYDDKHVSETNIKSQEKFLQHDLLFK--INGS
                                                             176 GGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLY 231
   Gaps
                                                                                                      GGDIVKGYVKYHNDDEQNVEYDFYNLNGEYGYEVLKMYADNKTINRDKLHLDIYLF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 9.1%; Score 113; DB 2; Length 232; Local Similarity 24.5%; Pred. No. 0.065; nes 59; Conservative 29; Mismatches 79; Indels
   18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ELQRNALSNIRQIYYYNEKAITEN--KESDDQFLENTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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   16, Mismatches
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   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : |:::
118 GRLIEKNVYV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 EKKVPINLWI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KUR>
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A;Molecule type: DNA
A;Residues: 1-62 «KUR»
A;Croserreferences: UNIPROT: 099TP8; GB:BA000018; PID:g13701399; PIDN:BAB42693.1; GSPDB:GCGentics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-235 <GOS>
A;Cross-references: UNIPROT:P13380; GB:M35514; NID:g153820; PIDN:AAA27017.1; PID:g153821
C;Superfamily: enterotoxin B
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A99758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KVRNYLLKHKNLYEFNS--SPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYND 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 TEEKKVPINLMIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDS--FGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 QARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 FIITVILISTYFTYHQSDSKKDISNVKSDLLYAYTITPYDYKDCRVNFSTTHTLNIDTQK 70
2 KKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFD-IPTNKKNITAQEIDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 FLENTLLFKGFFTGH-----TNK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                    exotoxin C precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A30509
R;Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A;Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A;Reference number: A30509; MUID:88314303; PMID:3045005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 KVORGLIVFHSSEGSTVSYDLFDA--QGQYPDTLLRIYRDNKTINSENL-HIDLYL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 183.5; DB 2; Length 235; 25.8%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 144; DB 2; Length 62; 39.3%; Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Mismatches 73; Indels
                                                                                                                                                                                                                                                          |||: |::::::|
119 NKTVESKSINVEVHL 133
                                                                                                                                                                                                                          216 NKTINSENLHIDLYL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 25.88 Matches 61; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: enterd
C;Keywords: exotoxin
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Db 36 ETQRKYXINMLHQYYSEESFESTNISVKSEDYYGSNVLINFRVFLLG 88 Qy 68 LVDLGSKDATKKGKK	Lancet 357, 1225-1240, 2001 A;Rile: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; WUDD:21311952; PMID:11418146 A;Accession: B8992 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-234 <kurs 0.27;="" 105.5;="" 11="" 13;="" 23.3%;="" 234;="" 2;="" 35;="" 54;="" 65;="" 70="" 79;="" a;experimental="" a;gene:="" b:="" best="" c;genetics:="" c;superfamily:="" conservative="" db="" dlrkkselqrnalsnlrqiyynbkatinesdoflentllfkgfftghpwnndllvd="" gaps="" indels="" length="" local="" match="" matches="" mismatches="" n315="" no.="" pred,="" query="" qy="" s#;="" score="" shock="" similarity="" source:="" strain="" syndrome="" th="" toxic="" toxin="" tst="" ="" <=""></kurs>
A; Residues: 1-234 *BLO> A; Cross-references: UNIPROT: P06886; GB:J02615; NID:g153122; PIDN: AAA26682.1; PID:g153123 A; Accession: B24606 A; Molecule : Wrype: protein A; Residues: 41-106;199-224 *BLO2> A; Note: the authors translated the codon ACT for residue 20 as Ile and GGG for residue 1 C; Superfamily: toxic shock syndrome toxin C; Keywords: toxic, shock syndrome; toxin E;1-40/Domain: signal sequence #status predicted <sig> F;41-234/Product: toxin shock syndrome toxin-1 #status experimental <mat> C; Newyords: toxic, shock syndrome toxin-1 #status experimental <mat> P;41-234/Product: toxin shock syndrome toxin-1 #status experimental <mat> Conservative 35; Mismatches 69; Indels 73; Gaps 12; Matches 53; Conservative 35; Mismatches 69; Indels 73; Gaps 12; Matches 53; Conservative 35; Mismatches 69; Indels 73; Gaps 12; Db SB DTFTNSEULDNISURGYNTERATENERSDDFLENTILFRGFFTGHPWYNDILUD 70 </mat></mat></mat></sig>	RESULT 28 E890LT 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E890ST 28 E80ST 28 E890ST 28 E80ST 28 E890ST 28 E8
RESULT 27 B89992 toxic shock syndrome toxin-1 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: B89992 R;Ruroda, M.; Ohtiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	Qy 59 TGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACM 107

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S. John Serzin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C. Species: Haemophilus influenzae
A. Variaty: strain SB29
A. Variaty: strain SB29
C. Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C. Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C. Date: 19-Mar-1997 #sequence_revision D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E. Miol. Microbiol. 19, 575-586, 1996
A. Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes. A. Reference number: S70901; MUID:96228706; PMID:8830248
A. Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain ILI: C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Accession: G86903
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. ll, 731-753, 2001
A;Fitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg A;Feference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT;Q9CDI9; GB:AE005176; PID:g12725299; PIDN:AAK06329.1; GSPDB:G?
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                       66 DLLVDLGSKDATNKYKG-----KKVDLYGAYYGYQCAGGT--PNKTACMYGGVTLHDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 -GRVTQVNKNSSKVALLSSSKGIDNKIPVRIESDGSPIYGILSSYDSQQEAYVVKNIDSQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 NRLTEEKKVPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|| |: || |: | |::|| |: || |::|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
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| TREPSSWNDTLVIDSGSKD--------GLTTGMIVMANGGVV---
                                                                                                                                 NEKDLRK--KSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYN
                                                                                                                                                                                                   33 NOKSVNKHDKEALYR-----YYTGKTMEMKNISALKHGKNNLRFK--FRGIKIQV
                                                                                                                                                                                                                                                                                                                                                                      81 LLPGNDKSKFQQRSYEGLDVFFVQEKRDKHDIFY---TVGGVIQNNKTS----GVVSAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 -----PWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 NNRLTE------EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 NALSNIRQIYYYNEKAIT----ENK---ESDDQFLENTLIFKGFFTGH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 ARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GKFKNGDSVFTSGLGTNSG----SQGGTPSGLL 249
                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91;
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                                                 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 7.6%; Score 94.5; DB 2;
Local Similarity 20.7%; Pred. No. 2.8;
nes 48; Conservative 26; Mismatches 67;
            Pred. No. 1.5;
                                                 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GKVQRGLIVPHSSEGSTVSYDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 GRVKISL----KDGSFYNLDL 201
        26.7%;
                                             54; Conservative
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: G86903
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Decession: G89807

R;Kuroda, M.; Ohita, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohita, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
M; Kuroda, M.; Ohita, T.; Hattoxi, M.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattoxi, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89807
A;Statuse trype: DNA
A;Residues: preliminary
A;Molecule trype: DNA
A;Residues: 1-227 <KUR>
A;Accession: G89807
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-231 «KUR»
A;Cross-references: UNIPROT:Q99WH6; GB:BA000018; PID:g13700317; PIDN:BAB41615.1; GSPDB:
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 TLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LDFERMADVINSEQI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EKSEEINE----KDLRKKSELQRNALSNLR-QIYYYN-EKAITENKESDDQFLENTLLFK 55
                                                                                                                                                                                                                                                                                                                                                                              exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 99.5; DB 2; Length 231; 24.0%; Pred. No. 0.82; tive 31; Mismatches 93; Indels 5:
                    Superfamily: toxic shock syndrome toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.0%
Matches 56; Conservative
                                                                                                                                     223 -NLHIDL 228
                                                                                                                                                                                                                225 KNIEVNĽ 231
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DB 2; Length 227;

7.8%; Score 96;

Query Match

A:Residues: 1-631 <loo> A;Cross-references: UNIPROT:Q48041; EMBL:U15055 A;Experimental source: strain SB29, clone DS-1090-3-2 R;Loosmore, S.M. submitted to the EMBL Data Library, September 1994 A;Reference number: S73320 A;Scession: S73321 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-250,'L',252-349,'RTDATTN',357-631 <low> A;Residues: 1-250,'L',252-349,'RTDATTN',357-631 <low> A;Across-references: EMBL:U15055, NID:g1223948; PIDN:AAC43931.1; PID:g1223949 A;Experimental source: strain SB29, clone DS-1090-3-2</low></low></loo>	Db 66LYDRYSKDTIN
-dependent	RESULT 34 (8990LT 34 (8990LT 34) (9990LE 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 (5)Accession M.; Ohtea, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch May, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seklmizu, K.; F
31 YY 31 YY 202 YN 68	Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-226 *KUX> A;Accesidues: 1-226 *KUX> A;Accesidues: TAZBARA1610.1: GSPDB:GY A;Accesidues: TAZBARA1610.1: GSPDB:GY
109 GGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEV	A.Experimental source: strain N315, C.Genetics: A.Gene: set6 C.Superfamily: toxic shock syndrome toxin
QY 151 TVQELDKFG 168 	Query Match Best Local Similarity 22.5%; Pred. No. 2.2; Matches 49; Conservative 38; Mismatches 63; Indels 68; Gaps 11;
Qy 169 LYNSDSFGGK 178 : : Db 429 MYYEDPLNGE 438	Qy 8 NEKDLARKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
RESULT 33 C89803 hypothetical protein SA0357 [imported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus C.Species: Staphylococcus aureus C.Species: O.May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C.Accession: C89803	Qy 64YNDLLVDLGS-KDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVT 112
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogudma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.	Qy 161 HYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDL 198
A; Reference number: AB9/28; MULD: 21311952; FMLD: 11418148 A; Accession: C89803 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-203 < KUR> A; Residues: U-203 < KUR> A; Residues: U-203 < KUR> A; Escoss-references: UNIPROT: Q99WK7; GB: BA000018; PID: G13700284; PIDN: BAB41582.1; GSPDB: C; Genetics: C; Genetics: A30357 A; Gross-Robertics: A30357 A; Gape: SA0357	RESULT 35 DVZQF multidrug resistance protein - malaria parasite (Plasmodium falciparum) N.Alternate names: P-glycoprotein C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004 C;Accession: S18204; A3254; XEMP, D.J.; Cowman, A.F.
Query Match 7.6%; Score 94; DB 2; Length 203; Best Local Similarity 21.5%; Pred. No. 1.9; Matches 51; Conservative 34; Mismatches 52; Indels 100; Gaps 12;	Mol. Cell. Biol. 11, 5244-5250, 1991 A,Title: Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum P. A.Reference number: S18204; MUID:92017800; PMID:1922044 A,Accession: S18204; MUID:92017800; PMID:1922044 A,Accession: S18204; MUID:9207, Acid sequence not shown: translation not shown
QY 1 SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG 60 ::	A; Molecule type: DNA A; Residues: 1-1419 <tri>A; Residues: 1-1419 <tri>A; Cross-references: UNIPROT: P13568; EMBL: X56851; NID: 99935; PIDN: CAA40180.1; PID: 99936 A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, December 1990 R; Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.</tri></tri>

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files
flagellar book protein FlgE homolog lmo0697 [imported] - Listeria monocytogenes (strain E C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: All161 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: All161 #Sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: All161 # Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, S.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authores: Kreft, J.; Kunh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Attle: Comparative genomics of Listeria species
A;Title: Comparative genomics of Listeria species
A;Title: Comparative genomics of Listeria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
C;Accession: Acissa
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

    B. subtilis YjbK protein homolog lin0964 [imported] - Listeria innocua (strain Clip11262)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: uncharacterized stand-alone CYTH domain protein, gram-positive bacterial
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                           LHDNNRLTEEKKVPIN-LWIDGKOTTVPI-DKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AL592022; PIDN:CAC96195.1; PID:g16413423; GSPDB:GN00178
A;Experimental source: strain Clip11262
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                                                                                                                                                                                                          ---NIKNANLINIKINNCL 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 KKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 FYLD-TADFGLKERNSALRIRKLETQ-----YQLTLKTPEARGLM-----ETTQILAAD 85
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                                                                                                                                                171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLYL
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                                                                                                                                                                                    1 Similarity 22.4% 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Act complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
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A,Experimental source: strain UAB CTIP
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                                                                                                              AMOJECUIE LYPE: mRNA
A,ROJECUIE LYPE: MRNA
A,ROJECUIE LYPE: GRONO
A,ROSIGUES: 1-1419 <FGOO
A,COSS-TECEFORCES: GBNZ9154; GB:M24322; NID:g160398; PIDN:AAA29646.1; PID:g160399
A,COSS-TECEFORCES: GBNZ9154; GB:M24322; NID:g160398; PIDN:AAA29646.1; PID:g160399
C,Superfamily: multidrug resistance protein; ATP-binding cassette homology
C,Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane profession and ATP-binding cassette homology <ABC1>
F,336-638/Domain: ATP-binding cassette homology <ABC1>
F,413-420/Region: nucleotide-binding motif A (P-loop)
F,583-587/Region: nucleotide-binding motif B
Cell 57, 921-930, 1989
A;Title: Amplification of the multidrug resistance gene in some chloroquine-resistant
A;Reference number: A32547; MUID:89288297; PMID:2701941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1134 RYISRPNVPIYKNLSFTCDSKKTTAIVGETGSGKSTFMNLLLRFYDLKNDHIILKNDMTN 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KSEEINEKD-----YYYN--EKAIT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 -ENKESDDQFLENTLLFKGFFTGHP------WYNDLLVDLGS------TDA----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trae-like protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SEEINEKDLRKK-SELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Indels
                                                                                                                                                                                                                                                                                                                                                                                  F;1144-1387/Domain: ATP-binding cassette homology <ABC2>F;1161-1168/Region: nucleotide-binding motif A (P-loop)F;1332-1336/Region: nucleotide-binding motif B
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23.1%; Pred. No. 21;
tive 41; Mismatches
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Best Local Similarity 23.1*
Matches 56; Conservative
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Best Local Similarity 21.84
Matches 65; Conservative
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A; Residues: 1-853 < KUR>
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Gene: MYPU 3830
Genetic code: SGC3
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hypothetical protein UU495 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82884
B;Bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A;Reference number: A82870
A;Reference number: A82884
A;Reference number: A82884
A;Reterence number: B2003
A;Residues: preliminary
A;Residues: 1-5005 <GLA>
A;Cross-references: GB:AE002148; GB:AF222894; NID:g6899495; PIDN:AAF30907.1; GSPDB:GN001;
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU495
A;Gene: UU495
A;Genetic code: SGC3
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Recession: G71615
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-679 cGAR>
A;Residues: 1-679 cGAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSD------SFGGKVQRGL 183
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1494 VNKLDQTNLISLQNFSFSNLKPNHLYRLLKVVYGDEQNFDAINEQKNILALNPSLVNSSF
                                                                       194 ----DNAGGKHKLQVNMKAATPDASGNVSYEYEIQMDGKALTPPVTGTLNYNAQGELTNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 TGHP-----WYNDLLVDLGSKDATNK-YKGKKVDLYGAYYGYQCAGGTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 90; DB 2;
Pred. No. 2.3e+02;
    170 YNSDSFGG--KVQRGLIVFHSSEGSTVSYDL--
                                                                                                                                                                                                                 251 ALKNI-QINSTVNGKQVNMGLNL 272
                                                                                                                                                                   TLLRIYRDNKTINSENLHIDLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
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Best Local Similarity
Matches 62, Conserva
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A;Experimental source: strain Clip11262
C;Genetics:
                                                                                            A;Molecule type: DNA
A;Residues: 1-411 <GLA>
A;Cross-references: UNIPROT:Q92DV7; GB:NC_003210; PIDN:CAC98775.1; PID:g16410086; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 YKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK------ 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 -----KVPINLWIDGKQT-----TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 -----KVPINLWIDGKQT-----TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---DNAGGKHKLÓVNMKAATPDASGNVSYEYEIQMDGKALTPPVTGTLNYNAQGELTNPD 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 YKKQSVVFN----DLLYQNTMGSVAGGLYAGTNPMSFGSGSKIGAILTDYTAGSPTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 YNSDSFGG--KVQRGLIVFHSSEGSTVSYDL--------PDAQGQY--PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 YNEKAITENKESDDQFLENTL--LFKGFFTG-HPW-----YNDLLVD--LGSKDATNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
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                                                                                                                                                                                                                                                                                                                                                                        Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
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                                                                                                                                                                                                                                                                                                                                                                    ch 7.3%; Score 90; DB 2; 1 Similarity 20.9%; Pred. No. 10; 55; Conservative 39; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALKNI-QINSTVNGKQVNMGLNL 272
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Matches 55; Conservative
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Best Local Similarity
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                                                          Status: preliminary
Molecule type: DNA
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us-09-900-766-7.rpr

Qy 72 GSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP 126 Db 670 VVNQGTNNYPLDRYKTS	RESULT 43 C8988 hypothetical protein SA1011 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #text_change 09-Jul-2004 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: C8988 R;Marcada, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146	Accession: CB9888 A;Accession: CB9888 A;Accession: CB9888 A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-21 kCMPs A;Cross-references: UNIRROT:Q99UU1; GB:BA000018; FID:g13700967; FIDN:BAB42263.1; GSPDB:GR A;Experimental source: strain N315 C;Genetics: A;Genetics: A;	Qy 63 WYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYG 109	sphc osph icte ' T2>	R.Theologis, A.; Becker, J.R.; Paul, C.J.; Federaplel, N.A.; Kaul, S.; White, U.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Zazo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Jauthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Eraser, C.M.; Venter, J.C.; Davis, R.W. A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Query Match 7.2%; Score 89; DB 2; Length 679; Best Local Similarity 19.7%; Pred. No. 23; Matches 53; Conservative 36; Mismatches 108; Indels 72; Gaps 9; Qy 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTL 52 Db 177 SEKEETENKNEETSNYNSNLANBINKICKYNLDQTDILLDDSNSERRNSKFKIKNTN 234 Qy 53 LFKGFFTGHPWYNDLLV-DLGSKDATNKY	Qy 97 AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELD 156 Db 290DNATLDLNVHTYMSLGMSILCKYSLLYCGKXNHIPRDPYTPFKKFVSILSLD 341 Qy 157LQARHYLHGK	merase (EC 2.7.7.7) family B, intein containing precursor unclease (EC 3.1) Fluid by endonuclease (EC 3.1) Fcus jannaschii sequence_revision 13-Sep-1996 #text_change 13-Sep-1998 O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.sek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Gl.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. (3, 1996) C.M.; Smith, H.O.; C.	A; Reference number: 864300; MUID: 96337999; PMID: 8688087 A; Accession: E64410 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1.1634 < BUL.> A; Rcoss-references: GB: U67532; GB: L77117; NID: 91591559; PID: 91591563; TIGR: MJ0885; A; Genetics: A; Map position: REV816304-811400 A; Start codon: TTG C; Function: Appl.> A; Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA	C; Function: <en1> A; Description: as DNA endonuclease PI-MjaI, catalyzes the hydrolysis of internal phospho A; Description: as DNA endonuclease PI-MjaI, catalyzes the hydrolysis of internal phospho C; Function: as DNA endonuclease PI-MjaII, catalyzes the hydrolysis of internal phosph C; Superfamily: DNA-directed DNA polymerase KOD C; Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing C; Superfamily: DNA-directed DNA polymerase family B extein 1 #status predicted <xt1> F; 1-425, 795-882, 1359-1634/Product: DNA-directed DNA polymerase family B extein 1 #status predicted <xt1> F; 795-882, Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <xt2> F; 883-1358/Product: DNA endonuclease PI-II (pol B intein 2) #status predicted <xt3> F; 883-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3> F; 1358-1634/Domain: DNA-directed DNA polymerase family B extein 5 #status predicted <xt3< td=""><td>F;425-795/Cross-link: peptide (Arg-Ser) #status predicted F;882-1359/Cross-link: peptide (Asn-Ser) #status predicted Cuery Match Query Match Best Local Similarity 2:1%; Pred. No. 68; DB 2; Length 1634; Matches 51; Conservative 34; Mismatches 80; Indels 66; Gaps 10; Qy 12 LRKKSELQRNALSNLRQIYYYNEKAITENKESDDGFLENTLLFRGFFTGHPWYNDLLVDL 71 Cy </td></xt3<></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt3></xt2></xt1></xt1></en1>	F;425-795/Cross-link: peptide (Arg-Ser) #status predicted F;882-1359/Cross-link: peptide (Asn-Ser) #status predicted Cuery Match Query Match Best Local Similarity 2:1%; Pred. No. 68; DB 2; Length 1634; Matches 51; Conservative 34; Mismatches 80; Indels 66; Gaps 10; Qy 12 LRKKSELQRNALSNLRQIYYYNEKAITENKESDDGFLENTLLFRGFFTGHPWYNDLLVDL 71 Cy

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C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Jo-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07067
A;Godt, D.B.; Proitsch, P.
Plant Physiol. 115, 273-282, 1997
A;Title: Regulation and tissue-specific distribution of mRNAs for three extracellular in:
A;Reference number: Z15897; MUID:97451780; PMID:9306701
A;Recession: T07067
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: 1-241 «GOD»
A;Residues: 1-241 «GOD»
A;Cross-references: UNIPROT:P93199; EMBL:X91389; NID:g1771149; PIDN:CAA62734.1; PID:g1771
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Tile: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 IKPNNNPLIVPDNSINRTEFRDPTTAWAGQDGLWRILIASMRKHRGMALLYRSRDFMKWI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OARHYLHGKFGLYN---SDSFGGKVORGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 KAQHPLHSSTNTGNWECPDFFP-----VLFNSTNGLDVSYRGKNVKYVLKNSLDVARF 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Listeria monocytogenes; Date: 27-Nov-2001 #text_change 09-Jul-2004; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #sequence_revision 27-Nov-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 KYKGKKVDLYGAYYGYQCAGGTP-NKTACMYGGVTLHDNNRLTEEKKVPINL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Indels
                                               beta-fructofuranosidase (EC 3.2.1.26) LINS - tomato (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 87.5; DE 21.9%; Pred. No. 8.2; tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.5; D
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: LINS
C;Superfamily: beta-fructofuranosidase
C;Keywords: cell wall; glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 I--DGKQTTVPIDKV-KTSKKEVTVQELD-
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21.1%;
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Best Local Similarity
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A;Variety: ATCC 29342
C;Date: 1:5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: 873438
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: 873327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-672 <HIM>
Cross-references: UNIPROT:P75072; EMBL:AE000013; GB:U00089; NID:g1673762; PIDN:AAB9576
Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                 A;Map position: 1
C;Superfamily: Pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructoki
                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                            74 KDAŢNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVT------LHDNNRLTEB 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 IN----NDLRLKLGYTKEDNVRTRAGLFRALEVSFGNYRAWTFYITLLGWKDTTEKIFKK 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YGYQCAGGTPNKTACMYGGVTLHDNN 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
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                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AE005173; NID:g6642673; PIDN:AAF20253.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MG032 homolog B01_orf672 - Mycoplasma pneumoniae (strain ATCC 29342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; Score 88; DB 1; Length 672; llarity 20.6%; Pred. No. 27; Conservative 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                              Length 617;
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                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                              7.1%; Score 88; DB 30.2%; Pred. No. 24; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 KKVPINLWIDGKQTTVPIDKVKTSKK 148
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.4.
Best Local Similarity 30.4.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
A; Accession: E96793
                                                                                                                                                                A; Gene: F14G6.15
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215 DNKTINSENLHIDL 228
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A;Residues: 1-2167 <
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                                                                                                                                                                                                      C;Genetics:
A;Gene: VC1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: i-1014 «GAR»
A;Cross-references: UNIPROT:O96276; GB:AE001425; GB:AE001362; NID:g3845310; PIDN:AAC7197
A;Experimental source: clone 3D7
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Ju1-2004
C;Accession: H81277
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I
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                                                                                                                                               TGHPW--YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDN 116
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                                                                   -----SYDLFDAQGQY 205
                                                                                                                                                                                                                                                                                                                       424 LAKSTSNDNPVYYVQYAHARISSILRSGK-EQGLEVTKDADMSLLQTEAEYDLLKVLGEF 482
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                                                                                                                      81 K---GKKVDLYGA-YYGY------OCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPIN 128
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                                        22 ALSNLRQI-YYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY
                                                                                                                                                                                                      LWIDGKQTTVPIDKVKTSK---KEVT----VQELDLQARHYLHGKFGLYNSDSF----
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  73; Indels 111; Gaps
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F;677-742/Domain: dnaJ amino-terminal homology <DNJ>
  40; Mismatches
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23.2%; Pred. No. 50;
vative 36; Mismatches
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Best Local Similarity
Matches 52; Conserv
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cell wall-associated protein precursor wapA (B. subtilis) homolog lin0454 [imported] - Li
c[Species: Listeria innocua
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A,Experimental source: serogroup O1; strain N16961; blotype El Tor
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Accession: H82177
A; Exture: Preliminary
A; Molecule type: DNA
A; Residues: 1-476 < HEI>
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8

Gaps

49

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Wholecule type: DNA

"Residues: 1-630 <POUZ.

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"Reference number: 527138; MUID: 83129428; PMID: 6297792
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C;Keywords: mitochondrion
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A;Molecule type: DNA
A;Residues: 1-630 <FOIL>
A;Residues: 1-630 <FOIL>
A;Cross-references: UNIPROT:Q9ZZX1; EMBL:AJ011856; GSPDB:GN00017; MIPS:Q0070
A;Experimental source: strain FY1679, isogenic derivative of strain S288C
R;Foury, F.; Roganti, T.; Leorenier, N.; Purnelle, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA endonuclease al5-alpha - yeast (Saccharomyces cerevisiae) mitochondrion N;Alternate names: protein Q0070
C;Species: mitochondrion Saccharomyces cerevisiae
C;Date: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession S78650, S78651, $27138
R;Foury, F.; Roganti, T.; Lecrenier, N.; Purnelle, B.
Bubmitted to the Protein Sequence Database, December 1998
A;Reference number: S78634
                                                                                                                2 EKSEEINEKD-----LRKKKSELQRNALSNLRQIY----YYNEKAITENKESDDQFLE
                                                                                                                                                                                                                                50 NTLLFK-----GFFTGHPWYNDLLVDLGSKDATN----KYK------GKKVDLYG
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                                                        55;
7.0%; Score 86.5; DB 2; Length 1751; 22.9%; Pred. No. 1.2e+02; ive 30; Mismatches 63; Indels 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 6.9%; Score 86; DB Local Similarity 19.5%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: SGD: AI5 ALPHA; SCAISalpha; MIPS: Q0070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain XL14-4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: SGD:S0007265
A.Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 241-630 <HEN>
A;Cross-references: EMBL:J01477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1251 YQELIPKVTTQE 1262
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                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 -----EVTVQE
  Query Match
Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S27138
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                                                                                                                                                                                                                                                                                                             probable periplasmic protein Cj0530 [imported] - Campylobacter jejuni (atrain NCTC 11168 C;Species: Campylobacter jejuni (cjpate: 31-Mar-2000 #text_change 09-Jul-2004 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: B81399 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyperence number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A45604

major blood-stage surface antigen Pv200 - Plasmodium vivax
C;Species Plasmodium vivax
C;Species Plasmodium vivax
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45604
R;Gibson, H.L.; Tucker, J.E.; Kaslow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C.;
Mol. Biochem. Parasitol. 50, 325-333, 1992
A;Title: Structure and expression of the gene for Pv200, a major blood-stage surface ant A;Reference number: A45604; MUD:92158013; PMID:1371329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9PHY4; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB7516
A;Experimental source: serotype O2, strain NCTC 11168
                                                                 1790 -TTYEYDAVNQLTKE-TLPD-----GTVKAYTYDGFGNRTQ---VAISGSETKTI 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: :: | :: | :: | :: | 556 BIHTQSDTASAKISSDNKEIHLKOLLSYIYRKHSNSSNSTFDIATNTQNISFGGANVALIL 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKLGPINAKNVYYKTLNFEDFNASVNDAYFKNNLLING---QTPXENDSPDIVKNKGIM 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNS- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLGSKDATNKYK----GKKVDLYGAYYGYQCAGGTPNKT-----ACMYGG----VTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TLAFDRVEADLKG---NALDLKGSRG-NAKFDLYYSS 653
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              OTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTV
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A,Status: Drahiminary
A,Molecule type: DNA
A,Residues: 1-1751 «GIB»
A,Cross-references: UNIPROT:Q26194, GB:M75674; NID:g160608; PID:g457336
A,Note: sequence extracted from NCBI backbone (NCBIN:83591, NCBIP:83592)
C,Superfamily: major merozoite surface antigen
C,Keywords: surface antigen
                                                                                                                                                                                 1835 DASYNDGNQLVSWNGEALTYDANG------NRTSDGK-----YTYT 1869
                                                                                                                            --SYD-------LFDAQGQYPDTLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 86.5; D
Local Similarity 22.9%; Pred. No. 48;
hes 58; Conservative 37; Mismatches
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14;

	### Residues: 1-1353 <#### CAD22 Cross-references: UNIPROT:Q9XW65; EMBL:AL033514; NID:e1343251; PIDN:CAD22 Experimental source: clone Y75B8A Senetics: Genetics:
RESULT 54 AG179 AG179 AG179 AG179 AG179 AG179 AG179 G)DOGAGABE HOMOLOG LIN2540 [Imported] - Listeria innocua (strain Clip11262) G)Species: Listeria innocua G)DAGE: 27-Nov-2001 #text_change 09-Jul-2004 G)DAGE: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 G)ACCESSION: AG1749 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. F; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jonnes, L.M.; Karst, U. Science 294 849-852, 2001 A;Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma A;Title: Comparative genomics of Listeria species. A;Title: Comparative genomics of Listeria species. A;Title: Comparative genomics of Listeria species. A;Accession: AG1749 A;Accession: AG1749 A;Accession: AG1749 A;Accession: AG1749 A;Residues: preliminary A;Residues: 1-1090 AG1A.	Db 506 HYMKLVERFVKTGALKKVYKKVRARATKKSKØMSEBDVRSEFDG 549 Qy 111 VTLHDNNRLTEBEKKVPINIMIDGKQTTVPIDKVKTSKKEVTVQ 153
A; Experimental source: UNIPROT: 092802; GB:AL592022; PIDN: CAC97767.1; PID: 916415062; GSPDB:GA; Experimental source: strain Clip11262 A; Experimental source: strain Clip11262 A; Experimental source: strain Clip11262 A; Experimental source: strain Clip11262 A; Experimental source: strain Clip11262 A; Ganetics: A; Gene: 1in2540 Query Match Best Local Similarity 22.5*; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; Pred. No. 72; P	synthetase (imported) - Listeria isteria innocua ar-2001 #sequence_revision 27-Nov-20170 Prangeul, L.; Buchrieser, C.; Amc Bernal, G.; Duchaud, E.; Durand, I. A.; Karst, U. S. 2001 A.; Karst, U. Simoes, N.; Tierrez, A.; Startive genomics of Listeria speciance: T.; Simoes, N.; Tierrez, A.; Amber: AB1077; MUID:21537279; PMII Minnary De: DNA - ESE «GLA» 1 source: strain Clip11262 1 source: strain Clip11262
RESULT 55 T27404 hypothetical protein Y75B8A.22 - Caenorhabditis elegans CjSpecies: Caenorhabditis elegans CjSpecies: Caenorhabditis elegans CjSpecies: Caenorhabditis elegans CjSpecies: Caenorhabditis elegans CjSpecies: Caenorhabditis elegans CjSpecies: T5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 CjAccession: T27404 R;Barlow, K. submitted to the EMBL Data Library, November 1998 A;Reference number: Z20361 A;Reference number: Z20361 A;Accession: T27404 A;Etextus: preliminary; translated from GB/EMBL/DDBJ	Query Match 6.9%; Score 85.5; DB 2; Length 556; Best Local Similarity 21.1%; Pred. No. 34; 74; Indels 111; Gaps 15; Matches 60; Conservative 39; Mismatches 74; Indels 111; Gaps 15; QY 22 ALSNIRQL-YYYNEKAITENKESDDOFLENTLIFKGFFTGHPWYNDLLVDLGSKDATNKY 80

Best Local Similarity 30.2%; Pred. No. 42; Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3; Qy 74 KDATNKYKGKKVDLYGAYYGYGAGGTPNKTACMYGGVTLHDNNRLTEE 122	RESULT 59 B44856 B44856 B44856 Batcocepin (EC 3.4.21.96) precursor [validated] - Lactobacillus paracasei (strain NCDO 18 Note to the names: cell-envelope-associated proteinase prtP; serine proteinase Lp151 (5, pecies: Lactobacillus paracasei (strain NCDO 18 Note to the note to the note of the note of the note of the note of the note of the note of the note of the note of the note of the note of the note of the note of the note of the note of note of the note of note of the note of note	A, Statuus: preliminary A, Molecule type: protein A, Molecule type: protein A, Residues: 189-196 (ANEA A, Cross-references: PIDN: AAB22052.1; PID: 9248666 A, Experimental source: strain NCDO 151 A, Note: sequence extracted from NCBI backbone (NCBIP: 94706) C, Genetics: A, Gene: prtP C, Superfamily: lactocepin; subtilisin homology C; Keywords: hydrolase; serine proteinase; transmembrane protein F; 1-23/Domain: signal sequence #status predicted <sig>F; 188-197/Domain: propeptide #status predicted <rro> F; 188-1902/Product: serine proteinase, cell-envelope-associated #status experim</rro></sig>	castor rophos
	RESULT 57 D86342 hypothetical protein F9H16.6 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004 C;Accession: D86342 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Denner, J.L.; J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Makin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Makin, R.; Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D86342 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-614 <stc> A;Kesidues: 1-614 <stc> A;Kesidues: 1-614 <stc> A;Kesidues: 1-614 <stc> A;Map position: 1 C;Superfamily: Pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phospho</stc></stc></stc></stc>	Query Match 6.9%; Score 85; DB 2; Length 614; Best Local Similarity 30.6%; Pred. No. 42; 3.42; Matches 26; Conservative 8; Mismatches 35; Indels 16; Gaps 3; Qy 74 KDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122 Db 412 KEGTYKGKKFNAICHFFGYQARGSLPSKFDCDYAYVLGHICYHILAAGLNGYMATVTN 469 Qy 123 KKVPINLWIDGKQTTVPIDKVKTSK 147 Db 470 LKSPVNKWKCGATPITAMMTVK 491	TESULT 58 T10102 diphosphate-fructose-6-phosphate 1-phosphotransferase (BC 2.7.1.90) alpha chain - diphosphate-fructose-6-phosphofructokinase (pyrophosphate) C;Species: Ricinus communis (castor bean) C;Species: Ricinus communis (castor bean) C;Species: Ricinus communis (castor bean) C;Species: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10102 R;Todd, J.F.; Blakeley, S.D.; Dennis, D.T. Genet 152, 181-186, 1995 Genet 152, 181-186, 1995 A;Accession: T10102 A;Accession: T10102 A;Reference number: Z16949; MUID:95137384; PMID:7835697 A;Accession: T10102 A;Reference number: Z16949; MUID:95137384; PMID:7835697 A;Accession: T10102 A;Residues: 1-617 <tod> A;Accession: T10102 A;Residues: 1-617 <tod> A;Coss-references: UNIPROT:Q41140; EMBL:Z32849; NID:9483546; PIDN:CAA83682.1; PIIC;Genetics: A;Introns: 30/3; 88/2; 126/1; 1151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 34C C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofic C;Keywords: phosphotransferase</tod></tod>

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erythrocyte membrane protein PfEMP3 PFB0095c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C;Accession: D71623 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C;Accession: D71623 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C;Accession: D71621 C; Zhou, L.; Sutton, Cummings, L.M.; Aravind, L.; Koonin, E.V.; Fertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MuID:99021743; PMID:9804551
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C980808
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizuteni-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hixamatsu, K.
Lancet 357, 1225-1240, 2001
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A;Cross-references: UNIPROT:096124; GB:AE001371; GB:AE001362; NID:93845092; PIDN:AAC7180:
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:BA000018; PID:g13700324; PIDN:BAB41622.1; GSPDB:GN
                                                                                                                            71 --LGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPIN 128
                                                                                                                                                                                       358 EMVGIVGATGSGKSTLAQLIPRLY-----DPTEGEVIIGGTNLKDINKKTLRSTVSFV 410
                                                                                                                                                                                                                                                                                                      129 LWIDGKQTTVPIDKVKTSKKEVTVQELD-----LQARHYLHGKFGLYNS-----DSFGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 ENLEEYNETÜLAKGKEVTNKARENLEE---YNETDLAKGKEVTNKARENL------ 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-2441 <GAR>
ALSNLRQI - - YYYNEKAITENKESDDQFLENTLLFKGF - - - FTGH - - PWYNDLLVD - - -
                                                       298 ALISLKRITEVLETEPDITYNENAPEODLEGTVEFRNVSFKYDGDDTPALEDISFKANVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.5; DB 2; Length 2
Pred. No. 2.6e+02;
9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exotoxin 15 (imported) - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900 EEYNE--TDLAKGKEVTNKAHENLEEYNETDLAKGKEV 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PWYNDLLVDLG-SKDATNK------YKGKKV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: set15
C;Superfamily: toxic shock syndrome toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-227 <KUR>
A;Cross-references: UNIPROT:Q99WG9;
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.6%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                178 -----KVQRGLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 GOKORLSITRĠVI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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22
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A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Sinces, M.; Tischeria, Species. A.; Tischeria species. A.; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                          Riffimmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
Nucleic Acids Res. 24, 4420-4449, 1996
A;fitle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: $73327; MUID:97105885; PMID:8948633
A;Accession: $73660
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P75278; EMBL:AE000031; GB:U00089; NID:g1674002; PIDN:AAB9598
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT: 0926Z5; GB:AL592022; PIDN: CAC98120.1; PID:g16415429; GSPDB: G
Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABC transporter, ATP-binding protein homolog lin2894 [imported] - Listeria innocua (stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 IKYTGGYQLYGFYAFAALFTKFPSSWSGEMNLKFIV----DGSIPVYTV--AKKDYPGSL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 FLENTLLFFKGFFTGHPWYNDLLVDLGSKDATNKYKGK-----KVDLYGAYYGYQCAGGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 NRTFSFLIAGFRTAIDWYYNAKKE--NNDAKQKAFGSQGIQFPKDGLNGIYMPDWLRGEL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 TSKS------NINLKIKELKVQNKIESPTINWIDG--VGIKQDKANPFNYRFEV-D 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 LDLQARHYLHGKF---GLYNS--DSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 PNKTACMYGGVTLHDNNRLTEEKKV-----PINLWIDGKQTTVPIDKVKTSKKEVTVQE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KSEEINEKDLRKKSELQRNAL----SNLRQIYYYNEKAITENKE-----SDDQ 46
                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                           MG288 homolog P02 orf509 - Mycoplasma pneumoniae (strain ATCC 29342)
C;Species: Mycoplāsma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Listeria innocua
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: Escherichia coli ABC transporter mdlA; ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LRIYRDN--------XTINSENLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%; Score 84.5; DB 2; Length 5
Best Local Similarity 22.5%; Pred. No. 37;
Matches 64; Conservative 35; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQ-FNDKDELLFTLYVKEQISVADPNFMNLLRGONLH-DLELVT
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6.8%; Score 84.5; DB
Best Local Similarity 23.3%; Pred. No. 43;
Matches 45; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Superfamily: hypothetical protein MG096
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Residues: 1-509 <HIM>
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Residues: 1-573 <GLA>
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                                                                                                                                                                  C;Accession: S73660
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A;Molecule_type: DNA
A;Residues: 1-492 -AADS-
A;Cross-references: UNDROT:O66746; GB:AE000690; NID:g2983100; PIDN:AAC06710.1; PID:g2983
A;Experimental source: strain VF5
C;Genteics:
A;Gene: g1pX
C;Superfamily: xylulokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-552 «KAM»
A;Cross-references: UNIPROT:092482; EMBL:L33180; NID:g3745835; PIDN:AAC63792.1; PID:g374:
A;Experimental source: isolate T3
C;Superfamily: Serratia marcescens chitinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 TTHYAVDALLEQGVDPNKIIVGVAMYGRGWTGVTNYTNGNYFSGTGNGPVSGTWEDG--- 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
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                                                                                                                                                                                                                                                                                                                                                                                                                                     66 DLL-VDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S ALMQDLRTEDIC-----RKLSEYSEYIKENT------GLLLHPYFSASK--- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 VPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGK--FGLYNS----DSFGGK 178
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3) C; Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV A; Variety: isolate T3 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: T41863 R; Gomi, S.; Majima, K.; Maeda, S. J. Gen, Virol. 80, 1323-1337, 1999 A; Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus A; Reference number: Z22020; MUID:99281911; PMID:10355780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 VQRGLIVFHSSEGSTVSYD-LFDAQG-QYPDTLLRIYRDNKTINSE-NLHIDLYLYT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-----HKTEPSNASRTLFNIKRLEYDDELLKIFRIPKNILPEVNESSSLFGYT 221
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                                                                                                                                                                                                                                                                                                                                                                        44 EQDPLELWEAVRKSLSBVIQQVGLKEINSIGITNQRE-----TVILWDKBTGRPVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 YNEKAI---TENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLY
                                                                                                                                                                                                                                                                                                                                  9 EKDLRKKSELQRNALSNLRQ---IYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYN
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                72;
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                                                                                                                                                                                                                             ch 6.8%; Score 84; DB 2; Length 492; 1 Similarity 25.7%; Pred. No. 39; 61; Conservative 30; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 84; DB 2; Length 552;
24.3%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Matches 45; Conserv
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                                                                                                                                                                                                                                  Query Match
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Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:09C118; GB:AE005176; PID:g12723243; PIDN:AAK04470.1; GSPDB:G
Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transposase of IS1077C [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23.Mar-2001 #sequence_revision 23.Mar-2001 #text_change 09-Jul-2004 C;Accession: D86671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: F70339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.; Young, W.G.; Lenox, A.L.; Graham,
                                                          10;
                                                                                                                                                                                                             63 WYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                                                                                                                                                          --NEKLTVKDDDEVSN-----VDVFVVREGSDKSAITTS----IGGIT-KTNGTQHKD 127
                                                                                                                                                                                                                                                                                                                123 KKVPINLWID---GKQTT-VPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                                                                                                                                                                                                                                                                                                          QRIMKKIGLRVTSYWHKSRK-----YNSYKGKVGTVAKN------KLHRRFR----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VPINLWIDGKOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ------TSIPHQKITTDTTEFKYYEDGIQKKCYLNPYIALFNSE------VI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|: :| :| | : | : | | ERVNKDELIEKEMLK-----IRQ------EHANAGYRPMRELLKQRGYHVNHKKV 62
                                                                                                                                                          81
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C;Species: Aquifex aeolicus
C;Bate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70339
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gral
                                                                                                             6 EINEKDLRKKSELQRN---ALSNLRQIYYYNEKAITENKBSDDQFLENTLLFKGFFTGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.8%; Score 84; DB 2; Length 272; Best Local Similarity 21.5%; Pred. No. 18; Matches 42; Conservative 30; Mismatches 67; Indels
     Score 84; DB 2; Length 227;
Pred. No. 15;
                                                                                                                                        90;
                                                          42; Mismatches
        6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYHISKQPSYQSIDI 158
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                                                          48; Conservative
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-272 <STO>
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A, Status: preliminary
A, Molecule type: DNA
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          Query Match
                                     Best Local
Matches 4
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Denicillin-binding protein mecA, low-affinity - Staphylococcus epidermidis
NyAlternate names: penicillin-binding protein 2'
C;Species: Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0774
R;Ryffel, C; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser, F.
Gene 94, 137-138, 1990
A;Fitle: Sequence comparison of mecA genes isolated from methicillin-resistant Staphylocc
A;Reference number: JQ0773; MUID:91033056; PMID:2227446
                                                                                                       A;Cross-references: EMBL:X63598; NID:946612; PIDN:CAA45141.1; PID:946613
C;Comment: Enzymes involved in cell wall synthesis are the primary target of beta-lactam
resistant Staphylococcus aureus" (MRSA) has a very low affinity to beta-lactam antibiotic
                                                                                                                                                                                                                                                                                                 A,Note: this resistance gene may have evolved by gene fusion; the amino end (pos 1-60) illin binding proteins from E. coli. The sequence Ser.X-Lys, conserved in penicillin epidding protein part is neither from S. aureus nor from E. coli C;Superfamily: penicillin-binding protein 2B C;Superfamily: penicillin-binding protein 2B C;Keywords: antibiotic resistance; cell wall synthesis F;403/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:054113; GB:X52592; NID:g46993; PIDN:CAA36828.1; PID:g46994
A;Experimental source: strain WT55
                                                                                                                                                                                                                                                A; Note: the gene for this protein contains a penicillin-inducable promoter, resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 NKESDDOFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDL----YGAYYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 6.8%; Score 84; DB 2; Length 668; Local Similarity 20.0%; Pred. No. 57; Onservative 45; Mismatches 87; Indels
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                         A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-41 <HIR>
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Matches 63; Conservative
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A; Residues: 1-668 < RYF>
A; Accession: S20574
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                                                                                   Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A)Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth A)Reference number: 222733; MUID:99278010; PMID:10348769
A)Accession: T44118
A)Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-245, 'G', 247-302, 'RV', 303-609, 'T', 611-668 <SON>
A; Residues: 1-245, 'G', 247-302, 'RV', 303-609, 'T', 611-668 <SON>
A; Cross-references: EMBL: Y00688; NID: g46629; PIDN: CAA66684.1; PID: g46629
B; Hiramatsu, K.; Asada, K.; Suzuki, E.; Okonogi, K.; Yokota, T.
FBBS Lett. 298, 133-136, 1992
A; Title: Molecular cloning and nucleotide sequence determination of the regulator region
A; Reference number: S20574; MUID: 92183847; PMID: 1544435
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A;Reference number: JQ0773; MUID:91033056; PMID:2227446
A;Accession: JQ0773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              penicillin-binding protein mecA, low-affinity - Staphylococcus aureus
N;Alternate names: MRSA PBP; penicillin-binding protein 2'
C;Species: Staphylococcus aureus
C;Date: 12-Feb-1993 #bequence revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0773; S00092; S20574
R;Ryffel, C; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser,
Gene 94, 137-138, 1990
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A; Cross-references: UNIPROT: Q53707; GB: X52593; NID: g46610; PIDN: CAA36829.1; PID: g46611
R; Song, M.D.; Wachi, M.; Dol, M.; Ishino, F.; Matsuhashi, M.
FEBS Lett. 221, 167-171, 1987
A; Title: Evolution of an inducible penicillin-target protein in methicillin-resistant & R: Reference number: S00092; MUID: 87304805; PMID: 3305073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GQ-----YPDTLLRI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSKKFEKGMKKLGVGEDIPSDYPFYNAQISNKNLDNEILLADSGYGQGEILINPVQILSI 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                         C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 NKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDL----YGAYYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 NKTLDDKTSYKIDGK-GWQKDKSWGGYNVTRYEVVNGNIDLKQAIESSDNIFFARVALEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Indels 120; Gaps
                                                                                                                                                                                                                                                                             A;Residues: 1-668 <ITO>
A;Cross-references: UNIPROT:Q54113; EMBL:D86934; PIDN:BAA82220.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 VQELDLQARHYLHGKFGLYNSDSFGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
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                                                                                                                                                                                                                                                                                                                              A Experimental source: strain N315
C Gentics:
A NOte: mecA
C Superfamily: penicillin-binding protein 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.8%; Score 84;
Best Local Similarity 20.0%; Pred. No.
                                                                             R; Ito, T.; Katayama, Y.; Hiramatsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| ||: :|
YSALENNGNINAPHL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y---RDNKTINSENL 224
  C;Species: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Conservative
                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                   C; Accession: T44118
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: : : : : : SEBLKQKRYKGYKDDAVIGKKGLEKLYDKKLQHEDGYRVTIVDDNSNTIAHTLIE	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-319 <par></par>
Qy 40 NKESDDQFLENTLLFKGFFTGHPWYNDLLGSKDATNKYKGKKVDLYGAYYGY 94 : : :	A;Cross-references: UNIPROT:Q9P152; GB:AL139075; GB:AL111168; NID:g6967817; FIDN:CAB/S099; A;Experimental source: serotype O2, strain NCTC 11168 C;Genetics:
95 QCAGGTPNKTACMYGGVTLHDNNRLTBEKKVP-INLWIDGKQTTVPIDKVKTSKKEVT	A; Gene: Cj0456c C; Superfamily: Campylobacter jejuni hypothetical protein Cj0456c
	Query Match 8.7%; SCOIE 83.2; DB 2; Length 319; Best Local Similarity 20.5%; Pred. No. 25; Matches 4R: Conservative 44: Mismatches 112: Indels 69: Gaps 12;
INVTRYEVVNGNIDLKQAIESSDNI PFARVALEL	2 EKSERINEKRINGKKERLORNALSNIRQIYYYNEKAITENKESDDOF 4
Qy 178KVQRGLIVFHSSEGSTVSYDLFDAQ	
Db 475 GSKKFEKGMKKGLGVGEDIPSDYPFYNAQISNKNLDNEILLADSGYGQGEILINPVQILSI 534	Qy 48 LENTLLFKGFFTGH-PWYNDLLVDLGSKATNKYKGKKVDLYGAYYG 93
535 YSALENNGNINAPHL	
RESULT 70	
T30545 major surface glycoprotein - Pneumocystis carinii (fragment)	148 KEVIVQELDEG
C;Species: Pheumocystis carinii C;Date: 22-0ct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001	
Cincebsion: 1993;3. R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A. Infect. Immun. 66, 4268-4273, 1998	278
A; Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari A; Reference number: 217905; MUID:98380374; PMID:9712777	
A;Accession: T30545 A;Status: preliminary; translated from GB/EMBL/DDBJ	T03276
A,Molecule type: DNA A,Residues: 1-1014 <abl:af038556; nid:g3560524;="" pid:g3560525;="" pidn:aac34980.1<br="">A,Cross-references: EMBL:AF038556; NID:G3560524; PID:G3560525; PIDN:AAC34980.1</abl:af038556;>	GAP protein - yeast (candida albicans) retrocramsposom poar C:Species: Candida albicans C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
A.Experimental source: f.sp. hominis C.Genetics:	C;ACCession: 1032/6 R;Matthews, G.D.; Goodwin, T.J.D.; Butler, M.I.; Berryman, T.A.; Poulter, R.T.M. J. Bacteriol, 179, 7118-7128, 1997
Ajerne: migi C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100	A;Title: PCal, a highly unusual Ty1/copia retrotransposon from the pathogenic yeast Candi A;Reference number: Z14877; MUID:98037512; PMID:9371461
Query Match Best Local Similarity 25.6%; Pred. No. 96; Matches 43; Conservative 25; Mismatches 70; Indels 30; Gaps 8;	A;Accession: T03276 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
Qy 2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLF 54	A; Kealdues: 1-324 <mat> A; CCOSS-references: UNIPROT:013307; EMBL:AF007776; NID:g2636718; PIDN:AAC49879.1; PID:g26 C;Genetics: A; Mobile element: retrotransposon pCal</mat>
Qy 55 KGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTA 105	Query Match 6.7%; Score 83.5; DB 2; Length 324; Best Local Similarity 25.8%; Pred. No. 25; Matches 42; Conservative 29; Mismatches 61; Indels 31; Gaps 10;
OY 106 CMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKE 149	Qy 1 SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLE 49
RESULT 71 C81390 hypothetical protein Cj0456c [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni	Qy 50 NTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYG 109 61 BFKYFHVAYPDVLEFLLDYNPKDKFKVKKVEGIYFTGWCLQWCLQ- 105 Qy 110 GYTLHDNNRLTBEKKVPINLWIDGKQTTVPIDKVKTSKKEVTV 152
C;Accession: C81390 R;Parkhill, X; Wreen, B.W., Mungall, K; Ketley, V.W.; Churcher, C. Basham, D.; Chillin R;Parkhill, X; Wreen, B.W. and A. S. Sarrell R; W. Vannyliet B. Whitehead, S. Rarrell	Db 106SIFDRFRLIMISKUPKHLQKBANLIKAAYDAV-TKSKDYTI 145
. н	RESULT 73 836595 L1 protein - human papillomavirus type 9 C;Species: human papillomavirus type 9

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LWIDGKQTTVPIDKVKTSKKEVTVQELD
                                                                                                           184
                                                                                                                                                    471 GOKORLSITRGVI 483
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A;Molecule type: DNA
A;Residues: 1-272 <STO>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-272 <ST2>
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Matches
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
D; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Ajtuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Ajtuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Ajtuthors Comparative genomics of Listerraz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ajtuthors number: AB1077; MUD:21537279; PMID:11679669
Ajtuti preliminary
Ajmolecule type: DNA
                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-507 <DEL.
A;Cross-references: UNIPROT:Q02480; EMBL:X74464; NID:g397068; PIDN:CAAS2488.1; PID:g3970
C;Superfamily: papillomavirus L1 protein
C;Keywords: late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC transporter, ATP-binding protein homolog lmo2751 [imported] - Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:Q8Y3T0; GB:NC_003210; PIDN:CAD00964.1; PID:g16412251; GSPDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: Escherichia coli ABC transporter mdlA; ATP-binding cassette homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NKTACMYGYQCAGGTP-----NKTACMYG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 GVTLHDNNRLTEEKKVPINLWIDGKQTTVPI-----DKVKTSKKEVTVQELDL----QAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTMDDRQNTSFDFK-QVQMFIIG---CIPCLGEHWDKAKVCEKDAN-NQLGLCPPIELR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPIN 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 LPDPNRFALADMSVYNPDKERLVWÁCRGIEIGRĠQPLGVGTSGHPLFNKVRDTENSSNÝQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 HYLHGKFGLYNSDSFG---GKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLR---IYR 214
                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                          -----ATNKYKGKKVD
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                    C;Accession: S36595
R;Delius, H.; Hofmann, B.
R;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
                                                                                                                                                                                                                                                                                                                              85;
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                                                                                                                                                                                                                                                                                     DB 2; Length 507;
                                                                                                                                                                                                                                                                                   6.7%; Score 83.5; DB 2; Length 5
20.3%; Pred. No. 44;
tive 38; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                          42 ESDDQFLENTLLF-----KGFFTGHPWYNDLLVDLGSKD-
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6.7%; Score 83.5; DE
Best Local Similarity 23.3%; Pred. No. 51;
Matches 45; Conservative 30; Mismatches
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                                                                                                                                 A; Accession: S36595
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transposase of IS1077F [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (species: Lactococcus lactis subsp. lactis subsp. lactis (c) species: Lactococcus lactis subsp. lactis (c) species: Lactococcus lactis subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. lactis (c) subsp. l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outer membrane usher protein cssD precursor - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: I83350
R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B.
FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of gense encoding coli-surface (CS) antigens in enterotoxigenic Escheric
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A;Cross-references: UNIPROT.P53512; EMBL:U04844; NID:g442375; PIDN:AAC45096.1; PID:g44237;
C;Superfamily: outer membrane usher protein fimD
C;Keywords: membrane protein
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A,Experimental source: strain IL1403
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166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 ISVSTDTDMYTPSEIDYTPEIHG-----VADSDSQIIVRQGNTIIINESVPAGPF 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 LGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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157 EKYFALLKVD-----KINGSTPDKAKERVLFENLTPLHPNERLIME------
                                                                                                                                                                                                                                                                                    22.6%;
                                                                                                                                                                                                                                                                                                           61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 QVQKGVSVTE
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les 62; Conserv
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Best Local Similarity
Matches 61; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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Best Local S:
Matches 62
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A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT: Q9K979; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB064
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000 .
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Spate: 10-May.2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 .
C;Accession: B89988
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                         7;
                                                                                         A;Molecule type: DNA A;Residues: 1-272 <ST3>
A;Residues: 1-272 <ST3>
A;Cross-references: GB:AE005176; PID:g12723748; PIDN:AAK04922.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: tra1077F; tra1077G; tra1077E
A;Cross-references: GB:AE005176; PID:g12725206; PIDN:AAK06245.1; GSPDB:GN00146
A;Experimental source: strain IL1403
A;Accession: H86727
                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 QRLMKKLGLRVTSYWHKSRK-----YNSYKGKVGTVAKN------KLHRRFR----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYLHGKFGLYNSDSFGGKVQRGLI 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein BH2771 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 NEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFK----GFFTGHPW
                                                                                                                                                                                                                                                                                                                                                                           19 ERVNKDELIEKEMLK-----IRQ-----EHANAGYRPMRELLKQRGYHVNHKKV
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                                                                                                                                                                                                                                            Length 272
                                                                                                                                                                                                                                                                                         67; Indels
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                                                                                                                                                                                                                                          ; Score 83; DB 2;
; Pred. No. 22;
30; Mismatches 67
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Best Local Similarity 29.3%; Pred. No. 34;
Matches 27; Conservative 14; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 IPDLF-----NVCKGROVLIVARYAGFE 186
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144 SYHISKOPSYOSIDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 VFH-SSEGSTVSYDL 198
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 21.5%;
Matches 42; Conservative 3
                                                                           Status: preliminary
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89986
A;Status: preiminary
A;Molecule type: DNA
A;Residues: 1.381 <KUR>
A;Cross-references: UNIPROT:Q99SS8; GB:BA000018; PID:g13701758; PIDN:BAB43051.1; GSPDB:GR
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Chlamydia trachomatis
C;Date: 13-5ep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: A71509
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Fitle: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track
A;Fitle: Genome sequence of A11570; MUID:99000809; PMID:9784136
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A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain UW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GHPWYNDLLVDLGSKDATNKYKGKK-----VDLYGAYYGY---QCAGGTPNKTACWYGGV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GKOTTVPIDKVK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription termination factor - Chlamydia trachomatis (serotype D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 FLIGEGVLEVLPDGFGFLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIVGTIRSPKEK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 EKDLRKKSELOR-NALSNLRQIYYYNEKA----ITENKESDDOFL--ENTL--LFKGFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NHP----LLADLGIKNAGLRLKFLKSETSGVAVWGKIYGEIKGQLDAAFSEETAI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                 6.7%; Score 83; DB 2; Length 381; 2.6%; Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 TSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 S--EGSTVSY------DLFDAQGQY 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: transcription termination factor C;Keywords: transcription termination
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A; Molecule type: DNA A; Residues: 1-241, 'P', 243-42, A; Cross-references: EMBL:U15; A; Experimental source: strain C; Genetics: A; Gene: tbp2 C; Superfamily: bacterial path F; 1-17/Domain: signal sequent F; 18-631/Product: transferring 22 Matches Coury Match Best Local Similarity 22 Matches A; Gene: bp2 C; Superfamily: bacterial path F; 18-631/Product: transferring 22 Matches Awayez, M.J.; Chan Db 243 YYNEKAITENKESD C, H.P.; Redder, E Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy	AAK43237.1; GSPDB:C Gaps 12; KVDLX 88 KVTLQ 262 VP 139 TVQVP 312 SEGST 193 PSSS- 365	enzae (strain SB32 lange 09-Jul-2004 England, D.M.; Ha ae transferrin rec
Oy 134 KQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFCGKVQRGLIVFHSSEGST 1	A,Cross-references: UNIPROT: Q97U84; GB:AE006641; NID:GL3816563; PIDN:AAK43. C;Genetics: SS03139 A,Gene: SS03139 Query Match	SULT 81 SULT 81 SULT 81 SULT 81 OALO SPECIES: Haemophilus infill Variety: strain SB32 Variety: strain SB32 Variety: strain SB32 Variety: strain SB32 Variety: strain SB32 Variety: strain SB32 Loosmore, S.M.; Yang, Y.; I. Microbiol. 19, 575-586, Title: Cloning and express Reference number: S70910; Status: preliminary; nucle Molecule type: DNA Kesidues: 1-631 «LOO> Cross-references: UNIPROT; Experimental source: strai Loosmore, S.M. Experimental source: strai Loosmore, S.M. Reference number: S73320 Reference number: S73320 Reference number: S73320 Reference number: S73320

Db 468 SSILINKOLLAFYWNDLSIDMG-RESVSRYASLGDRANLYSLLYGKYYMTEKTNEASVPYG 526 Qy 110 GVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLH 164	C;Genetics: A;Gene: CAC1771 Query Match Query Match Best Local Similarity 22.2%; Pred. No. 21; Matches 52; Conservative 37; Mismatches 90; Indels 55; Gaps 11; Qy 5 EEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHP 62
RESULT 83 E71604 hypothetical protein PFB0870w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C;Accession: E71604 E;Accession: E71604 E; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Ressius: prefininary; nucleic acid sequence not shown; translation not shown A;Moolecule type: DNA A;Residues: 1-2380 cGAR> A;Coss.references: UNIPROT:096266; GB:AE001421; GB:AE001362; NID:g3845293; PIDN:AAC7196 C;Genetics: A;Gene: PFB0870w	Qy 123 KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYI-HGKFG- 168 128 KATKVVINNFIRTAQNDKFIDSGKQNTIVI-TIASSSKSINDESIDSSLEHYIKENKINA 186 Qy 169LYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRI 212
Duery Match 6.7%; Score 83; DB 2; Length 2380; Best Local Similarity 23.1%; Pred. No. 3.4e+02; 4atches 46; Conservative 25; Mismatches 68; Indels 60; Gaps 2 EKSERINEKDLRKKSELQRNALSNLRQIYY*NEKAITENKESDD 2 I:	A;Reference number: A89758; MUD:21311952; PMID:11418146 A;Accession: B89807 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-292 «KUR» A;Residues: 1-292 «KUR» A;Residues: 1-292 «KUR» A;Cross-references: UNIPROT:099WH8; GB:BA000018; PID:g13700315; PIDN:BAB41613.1; GSPDB:GR A;Experimental source: strain N315 C;Genetics: A;Gene: set9 A;Gene: set9 C;Superfamily: toxic shock syndrome toxin C;Superfamily: toxic shock syndrome toxin Query Match Best Local Similarity 20.3%; Pred: No. 27; Matches 51; Conservative 44; Mismatches 71; Indels 85; Gaps 13;
Db 182TKCKIEIANFISFYFFFLHIKDILNKNNDNGLMNKKKSSLKDICNIKYIYKKIKT 236 Qy 146 SKKEVTVQELDLQARHYLH 164 Db 237 SKKYISSNDMDTCIRNYLY 255 RESULT 84	Qy 6 BINEKDLRKKSELQRNALS
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	OY 106 CMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBLDLQARHYL 163

GSPDB:GN

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membrane conserved hypothetical protein SSO0195 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: P90160 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. A;Debription: Sulfolobus solfataricus complete genome.

A;Reference number: A99139
                                                                                                                                                                                                 C,Accession: H97273
R,Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J, Daly, M.J.; Bennett, G.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1.233 «KUR»
A;Cross-references: UNIPROT:Q97ER9; GB:AE001437; PIDN:AAK80979.1; PID:g15026099;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 -----TGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 WYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122
                                                                                                                hypothetical secreted protein [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :50 YYQNENDGNKLYK-IKTDGSDRQKLNDSYSSYITVVDNYIYYQ-----NETL----GNS
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260 KELSEKTSKKISEEKQKIIATIKQI----BDSIKDYEDKENNYRQLGNFILSKAY----
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Local Similarity 23.7%; Pred. No. 31;
hes 54; Conservative 43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 HYLH--GKFGLYNSDSFGGKVQRGL-----
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C;Superfamily: hypothetical protein YPL009c
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A,Status: preliminary
A,Molecule type: DNA
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A, Status: preliminary
A, Molecule type: DNA
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                                                                    C;Accession: C64716
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; WUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:026091; GB:AE000654; GB:AE000511; NID:g2314743; PIDN:AAD086d
C;Superfamily: rplA lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p-aminobenzoate synthase component I homolog - Haemophilus influenzae (strain Rd KW20) C; Species: Haemophilus influenzae (cjpate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C; Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C; Accession: F64187 # R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, FGCcayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, FGCcayne, J.D.; Frinc, L.D.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995 A; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Reference number: A64000; WUID:95350630; PMID:7542800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 RIIDLSNAAARDIDMVKKGTASVRLIVLGFGGVISTQYEQSFNASSSKILHKEFKVGESE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TTVPIDKVKTSKKEVT----VQELDLQARHYLHGKFGLYNSDSFGGKVQRGLI-----V 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| : || | :| :| | 237 TLLPAGSISGAPKEKTTQIIQQAEKQXRGYYTGIFGIFDGKTLQSAVAIRFISQVDEKFY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN-- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 --KTA-----CMYGGVTLHDNNRLTEEKKVPIN----LWIDGKQTTV------ 138
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                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                            C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | : : | | | | : | | | | : | | 31 SYKHESLRAYENAKDYDPTTKKAAYKRNFFER-----HFKRYSDSQDSNTKDQPLDNGMR
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rare lipoprotein A - Helicobacter pylori (strain 26695)
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6.7%; Score 82.5; DB
Best Local Similarity 27.3%; Pred. No. 31;
Matches 24; Conservative 16; Mismatches
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6.7%; Score 82.5; DB
Best Local Similarity 19.7%; Pred. No. 29;
Matches 59; Conservative 40; Mismatches
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A; Residues: 1-328 <TIGR>
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A; Residues: 1-315 < TOM>
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167 Query Match 167 Query Match 168 Query Match 168 Query Match 168 Query Match 168 Query Match 168 Query Match 168 Query Match 168 Query Match 168 Query Match 178 Query Match 188 Query Match 198 Query M		E. GODDE . CEDIDOC 1. DEDUCATO DE SECONDA DE DE CONTROL DE DESCRIPCIONES CONTROL DE CONT
м. В. (С.). (С	311 BIDQLLINNRAKSKKVKLNVDGVEIELDTSLSAT	A;CTOSB-TETETENCES: UNIFKUI:Q&ZHBU GB:ALDSVO842; FILN:CACGSOS7:1; FILV:SISS/SOC., OSFUE:OS C;Genetics: A;Gene: iutA
м. В. 111, 111, 111, 111,	123 KKVPINLMIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKF 16	Match 6.7%; Score 82.5; DB 2; Oscil cimilarity 95 1%; Dred No 83;
м. В. ОВ : С ОВ	545 NNA-TRKET DEALE INKOLEKALING LEBUNGKURAKLENKELENKUSI ALLUKUKUT.	nes 60; Conservative 20; Mismatches 72; Indels
м. в. 111, 111, 111, 111,	108 GLINSDSGGNVGGLIVE-RSSGSJVSILLE	51 TLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYY
M. B. 11, 11, W. B. 66.;	215	130 TSLYGGGSTGGLINIVIKKGQEGKQVELQLGGKTGFNSRNDADS
M.B. 0B:C M.B. 6G.)		102
M.B. 66.7 111, 70B:Q M.B.	RESULT 90 AH0340	152 VQELDLQARHYLHGKFGLYNSDSFGG
м. в. б. б. б. б. б. б. б. б. б. б. б. б. б.	putaive autotransporter protein yapC [imported] - Yersinia pestis (strain C092) C:Species: Yersinia pestis	225 VMGTGTLNIDENQQLQLTTQYFNSESDGKHGLYLGQNFSAVTGTGQASNSAALNSDRIPP
м. в. С	C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C.Accession: AH0340	178 KVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDLY :
. DB : G М. В 311,	R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Crohin, A.; Davise, R.M.; Davise, P.; Dougan, G.; il M. Rutharford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,	285
υВ:С М. В 3.11,	Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.	RESULT 92 D83845 Localstain markein Buleca (immarkeal) _ Bacillus halodurans (strain C-195)
	A;Keference number: AB0001; MUID:21470413; FMID:11586360 A;Accession: AH0340 A;Status: preliminary	Typourecrear process in anison temporated control of the control o
		C;Accession: D83845 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
	••	Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650; MUID:20512582; PMID:11058132
	6.7%; Score 82.5; DB 2; Length 638; imilarity 20.5%; Pred. No. 71;	A;Accession: D83845 A;Status: preliminary A;Molecule type: DNA
	; Conservative 22; Mismatches 64; Indels 81; Gaps	A; Kegldues: 1-520 <510> A; Cross-references: UNIPROT: Q9KCK7; GB: AP001512; GB: BA000004; NID: 910174030; PIDN: BAB052E
	68 LVDLGSKDATNKYKGKKVDLYGAYGYGYGGGTPNKTACMYGGVT :	A;Experimental Bource: strain C-125 C;Genetics: A;Gene: BH1564
	113	6.6%; Score 82; DB 2; Length 520; Similarity 27.5%; Pred. No. 60;
	354 APRHILNAELSTLRQRQGELKADAEGTVGVWARYLTDDSRLSDNKNIAFKNTLSGMEI	46; Conservative 23; Mismatches 58; Indels 40; Gaps
	139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLXNSDSFGGKVQRGLIVFHSSEGSTVSY	
	197	82 145
	ä	139
100,0000	AESULT 91 ABO122 probable ferric siderophore receptor iuta [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis	198 PDLLSFGTIIEPKVIÇAKELDDDHFL-DLYGLNDSYGTAVVRTLI
	C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C;Accession: AB0122 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, M.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, M.; Whitehead, S.; Barrell, il, M.; Stelton, J.; Stevens, M.; Whitehead, S.; Barrell, il, M.; Stevens, M.; St	RESULT 93 855243 upiquitin-like protein 8 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 10-oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
 .	Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB001; MUID:21470413; PMID:11586360 A;Accession: AB0122 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-726 <kur></kur>	CiAccession: S55243; Solubs R.Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D. Genetics 139, 921-939, 1995 A.Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like prote A.Reference number: S55242; MUID:95229071; PMID:7713442 A.Accession: S55243 A.Status: nucleic acid sequence not shown

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C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #text_change 09-Jul-2004 C;Date: 15-Oct-1999 #aequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T28156 M: T = Tanaka, M: Inselburg, J:; Bzik, D.J. Mol. Blochem: Parasitol. 61, 37-48, 1993 A;Fitle: Molecular characterization of the largest subunit of plasmodium falciparum RNA FA;Reference number: Z20478; MUID:94081864; PMID:8259131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2910 <FOX>
A;Cross-references: UNIPROT:Q26008; EMBL:L11172; NID:g414321; PID:g414322; PIDN:AAA72349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DNNRLTEEKKVPI------NLWIDGKQTT---VPIDKVKTS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 KK---EVTVQEL-DLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQ 202
                                                289 LADVYQIPEKRVHVILNGVDENGFTSDKKLRTLFRSKLGLPENSSAIVLGAAGRLVKDKG 348
                                                                                                 --LLFKGFFTGHPWYNDL-LVDLGSKDATNKYK--GKKVDLYGAYYGYQCAGGTPNKTAC 106
                                                                                                                                   401 FYNGIDLFVNPTLRPQGLDLTLMEAMLSGKPVMASRYASIKRTIVVNDEFGFMFAPNVEA 460
                                                                                                                                                                                                                                                                                                                                      107 MYGGVTLHDNNRLTEE-----PIDKV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed RNA polymerase homolog - malaria parasite (Plasmodium falciparum)
     ----- 51
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C;Species: Brevibacillus brevis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 04-Apr-2004
                                                                                                                                                                                                                                                                                                  144 KTSKKEVTVQE----LDLQARHYLHGKFGLYNSDSFGGKVQRGL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EKSEEINEKDIRKKSELQRNALSNIRQIYYYNEKAITENKESDD-----QFLENTLIF-
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                                                                                                                                                                                                                                                                                                                                                                                                   184 ----IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 6.6%; Score 82; DB 2; Length 2910; Local Similarity 19.7%; Pred. No. 5.2e+02; Local Si, Conservative 44; Mismatches 83; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T28156
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQY---PDTLLRIYRDNKTINSENL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 2840/3; 2880/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Robben, J.; Volckaert, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 QCAGGTPNKTACMYG---GVTLHDNNR------LTEEKKVPINLWIDGKQTTVPI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 PLEGG---RTLAHYNIQKGSTLYLVTRFRCGMQIFVKTLTRKR---INLEVESMDT---I 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KKEVTVQELDLQARHYLHGKFGL-YNSDSFG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKIIT-LEVLSSDTIKSVKAKIQDKVGSPPDQQILLFRGGQLQDGRTLGDYNIRNESTLH 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |: | :::: | : : : : : ::: |: | | ESSDII--ENVKAKIQDREGLRPDHQRLIFHGEELFTEDNRTLADYGIRNRSTLCLALRL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 GKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYR-----DNKTI-----NSENLH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 KG-----KVDLYGAYY-GY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T5K18.240 - Arabidopsis thaliana ($\text{C}$)$pecies: Arabidopsis thaliana ($\text{mouse-ear}$ cress)

C;$pecies: Appr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05829

R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volcl submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15453
                                                                                                                                                                                              A;Modecule type: DNA
A;Residues: 1.341, TE', 343-631 <CAW>
A;Residues: 1.341, TE', 342-631 <CAW>
A;Residues: BRBL:L05917; NID:g870793; PIDN:AAA68879.1; PID:g870794
C;Superfamily: ubiquitin homology <UBH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITE-NKESDDQFLEN-----TLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 82; DB 2; Length 631; 21.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 756;
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A;Residues: 1-756 <BEV>
A;Cross-references: UNIPROT:O49464; EMBL;AL022580
A;Experimental source: cultivar Columbia; BAC clone T5K18
C;Genetics:
                                                                                                      R.D.
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                                                                       A; Experimental source: ecotype Columbia
R; Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra,
Bubmitted to the EMBL Data Library, June 1995
A; Reference number: S61068
A; Accession: S61068
A;Molecule type: DNA
A;Residues: 1-631 <CAL>
A;Cross-references: UNIPROT:039256; EMBL:L05917
                                                                                                                                                                                                                                                                                                                         F;79-154/Domain: ubiquitin homology <UBH2>
F;155-237/Domain: ubiquitin homology <UBH3>
F;238-318/Domain: ubiquitin homology <UBH3>
F;319-392/Domain: ubiquitin homology <UBH5>
F;393-468/Domain: ubiquitin homology <UBH5>
F;465-551/Domain: ubiquitin homology <UBH5>
F;465-551/Domain: ubiquitin homology <UBH5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 21.0*
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 IDLYL 230
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A; Introns: 494/1
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Best Local Similarity 25.1%;
                                                                                                                                                                                                                                                                                                                                                                                    184 IVFHSSEGSTVSYDL 198
                                                                             20.0%;
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                                                                             Best_Local Similarity 20.08
Matches 27; Conservative
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Residues: 217 <ER2>
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                                                      Query Match
A;Gene: set8
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F;2583-3025/Domain: acyl carrier protein homology <ACE3>
F;2683-311/Domain: acyl carrier protein homology <ACE3>
F;3643-311/Domain: acyl carrier protein homology <ACE3>
F;361-4066/Domain: acetate-CoA ligase homology <ACE4>
F;4656-5104/Domain: acetate-CoA ligase homology <ACE5>
F;4656-5104/Domain: acetate-CoA ligase homology <ACE5>
F;5122-5190/Domain: acetate-CoA ligase homology <ACE5>
F;5122-5190/Domain: acetate-CoA ligase homology <ACE5>
F;5122-6147/Domain: acetate-CoA ligase homology <ACE6>
F;6165-6233/Domain: acyl carrier protein homology <ACE6>
F;6165-6233/Domain: acyl carrier protein homology caces
                            ;Mootz, H.D.; Marahiel, M.A.
- Bacteriol. 179, 6843-8850, 1997
- Fitle: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequ
:Reference number: Z20969; MUID:98012987; PMID:9352938
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A;Cross-references: UNIPROT:099WH9; GB:BA000018; PID:g13700314; PIDN:BAB41612.1; GSPDB:0
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 NDLLVD-LGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ETRLTOHE 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVPINLWIDGKQTTVPIDKVKT-----SKKEVTVQELDLQARHYLHGKFGLYNSD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    881 AV-----KEAVVIVEKDESGONVLYAYLVSERELTVAEL----REFLGRTLPSYMIP 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: A89807
                                                                                                                                                                                                                       Residues: 1-6486 <MOO>
Cross-references: EMBL:AF004835; NID:92623770; PID:92623773; PIDN:AAC45930.1
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A99807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GGKVQRGLIVFHSSEGSTVSYDLFDA-QGQYPDTLLRIYRDNKTINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 SELORNALSNIRQIY-----YYNEKAITENKESDDQFLENTLIFKGFFTGH--PWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6486;
                                                                                                                                                                                                                                                                                                                                                           Pathway: tyrocidine biosynthesis
Keywords: carrier protein; phosphopantetheine; phosphoprotein
510-950/Domain: acetate-COA ligase homology <ACL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exotoxin 8 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                              968-1036/Domain: acyl carrier protein homology <ACPl>1546-1987/Domain: acetate-CoA ligase homology <ACL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 82; DB 2; I 20.2%; Pred. No. 1.4e+03;
                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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KiErdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 266, 12090-12098, 1991
A,Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subur A,Reference number: A40457; MUID:91268092; PMID:2050703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-216,'A',218-616 <ERD>
A;Residues: 1-216,'A',218-616 <ERD>
A;Cross-references: UNIPROT:P27694; GB:M63488
A;Octe: parts of the sequence determined by protein sequencing
A;Note: this sequence has been corrected in reference A44501
R;Erdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 268, 2268, 1993
A;Title: Characterization of a CDNA encoding the 70-kDa single-stranded DNA-binding subur A;Reference number: A44501; MUID:93131993; PMID:8420996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Superfamily: replication protein Al
C:Kaywords: DNA replication initiation; single-stranded DNA binding; trimer; zinc finger
F;481-503/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cross-references: GDB:138362; OMIM:179835
Wap position: 17p13.3-17p13.3
Complex: Replication protein A is a trimer of 70K (A1), 32K (A2), and 14K (A3) chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HPWYNDLLVDLGSKDATNKYKCKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 BEKKVPINLWIDGKQTTVPI----DKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSF 175
                                                                                                                                                                                                                                                                        183
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                                                                                                                                       123
                                                                                                                                                                                                                                                                                                           262 ELSVTKKDNQGMISRDVSEYMITKERISLKELDFKLRKQLIEKHNLY-----GNMGSGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replication protein A1 - human
N:Alternate names: replication protein A 70K chain
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LSNLRQIYYY------NEKAITENKES-----DDQFLENTLLFKGFFTG
                                                                                                                                    64 YNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK
                                                                                                                                                                                                                                                                           124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL
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   Length 356;
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   DB 2;
6.6%; Score 81.5; I
(0.0%; Pred. No. 41;
.ve 31; Mismatches
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Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q98Q87; GB:AL445566; PID:g14089893; PIDN:CAC13652.1; GSPDB:G
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                               C; Accession: G90571
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A; Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                      hypothetical protein MYPU 4790 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLEBIKRIFKQKHKKEIEIWSKNIPHQ--GI-------GFDYIHNDEKHT---- 700
---GARVSD-F 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 KNYEQDNKDIRKISDDKLYNKIDLRFFLLEQWAKTKKIFYGNIKEEINNWLKFFIDQNFK 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 VPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein F53H1.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 804;
342 AKRNIYL-MDTSGKVVTATLWGEDADKFDGSRQPVLAIK-----
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                                                 GGKVQRGLIVFHSSEGSTV-----SYDL---FDAQGOYPD 207
                                                                                               GG---RSLSVLSS---STIIANPDIPEAYKLRGWFDAEGQALD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 81.5; DB 2;
18.5%; Pred. No. 1.1e+02;
iive 42; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KSEEINEKDLRKKSELORNALSNLR-
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-----SFPDFIIR 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-804 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: G88637
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Length 1378;
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6.6%; Score 81.5; DB 2; Length 1
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tive 41; Mismatches 100; Indels
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                        Best Local Similarity
Matches 54; Conserv
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Search completed: July 26, 2005, 11:08:47 Job time : 25 secs

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Minimum DB
Maximum DB
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Stap_Strp_tox_C; 1.
Pfam; PF01873; Stap_Strp_toxin; 1.
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PS00278; STAPH_STREP_TOXIN_2; 1.
PS00278; Staph_STREP_TOXIN_2; 1.
ture; Direct protein sequencing;
Superantigen; Toxin; Zinc.
EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                      HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
                                           SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
                                                      SEKSEBINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
               HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
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3 MEDLINE-96022987; PubMed=7552730;
3 MEDLINE-96022987; Purey W.F. Jr., Ple
4 Swaminathan S., Furey W.F. Jr., Ple
6 "Residues defining V beta specific "Residues defining V beta specific "Residues defining V beta specific "Residues defining V beta specific "Residues defining V beta specific "Residues defining V beta specific "Residues defining V beta specific"

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Name=entA; OrderedLocusNames=MW1889;
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01-JAN-1990 (Rel. 13,
25-OCT-2004 (Rel. 45,
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Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
J. Biol. Chem. 271:32212-32216 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95354648; PubMed=7628431;
Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M.,
Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=87222293; PubMed=3584106;
Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz
"Complete amino acid sequence of staphylococcal e
J. Biol. Chem. 262:7006-7013(1987).
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Betley M.J., Mekalanos J.J.;
"Nucleoride sequence of the type A staphylococcal enterotoxin gene.";
J. Bacteriol. 170:34-41(1988).
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Yamamoto K., Hiramatsu K.;
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COMPARISON OF STRUCTURE OF SEA AND SEC2.
MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
"A structural and functional comparison of staphylococcal enterotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 14:3292-3301(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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staphylococcal
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enterotoxin
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InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006123; Staph/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF02876; Stap Strp tox C; 1.
Pfam; PF01133; Stap Strp toxIn; 1.
PRINTS; PR00279; BACTRITOXIN.
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PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
3D-structure; Complete proteome; Direct protein sequencing; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
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SUBCULIULAR LOCATION: Secreted.

MISCELLANEOUS: This toxin seems to be coded by a bacteriophage. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
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%Ol. Biol. 269:270-280(1997). FUNCTION: Staphylococcal enterotoxins cause the intoxication 
staphylococcal food poisoning syndrome. The illness characterized 
braphylococcal food poisoning syndrome, shock, and in some cases
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D=25-257.
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Best Local S
Matches 191
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05-JUL-2004
05-JUL-2004
    EMBL; BX571857; CAG43678.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006123; Stap/Strep_toxin
                                                                                                                                                                                       PubMed=15213324; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitech E., Rutherford K.M., Sanders M.
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomes of two clinical Staphylococcus aureus evidence for the rapid evolution of virulence and drug proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=15213324; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=SAS1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterotoxin type A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6G7Y7;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Stap/Strep_toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.6%; Score 1023;
82.0%; Pred. No. 3
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1es 25;
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                                                                                                                                                                                                                                       Sanders M.,
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Best Local S
Matches 191
                                            EMBL; AP003364; BAB58110.1; -.

HSSP; P13163; 1L05.
G0; G0:0005576; C:extracellular; IEA.
G0; G0:000576; C:extracellular; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR008177; Bctrl tox.
InterPro; IPR008123; Stap/Strep_toxin.
InterPro; IPR008126; Staph/Strept tox.
InterPro; IPR008126; Staph/Strept tox.
InterPro; IPR008127; Staph tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF01123; Stap_Strp_tox.C; 1.
PRINTS; PR00279; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q931M4 PRELIMINARY;
Q931M4;
01-DEC-2001 (TrEMBLrel. 19, 0
01-DEC-2001 (TrEMBLrel. 19, 1
01-OCT-2003 (TrEMBLrel. 25, 1
Enterotoxin P.
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PROSITE; PS00277; STAPH_STREP_TOXIN_1;

PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=ML50 / ATCC 700699;

MEDLINB=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

KUITOda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Mhole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox.OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=sep; OrderedLocusNames=SAV1948;
Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Lancet 357:1225-1240(2001).
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257 AA;
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                             proteome.
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82.0%; Pred. No. 3.4e-76;
tive 17; Mismatches 25
     MW;
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Last sequence update)
Last annotation update)
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     15C2D36270FA8241 CRC64;
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                                                                                                                                                                                                               "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

REMBL; BX571856; CAG41028.1; -.

DR GO; GO:0005475; C:extracellular; IEA.

DR GO; GO:0005405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact endotox.

InterPro; IPR006127; Bact endotox.

DR InterPro; IPR006177; Bact fox.

DR InterPro; IPR006173; Staph/Strept_tox.

DR InterPro; IPR006126; Staph/Strept_tox.

DR InterPro; IPR006126; Staph/Strept_tox.

DR InterPro; IPR006173; Staph tox OB.

Pfam; PF01123; Stap Strp_tox C; 1.

DR Pfam; PF02876; Stap Strp_tox C; 1.

DR PRINTS; PR00279; BACTELTOXIN.

DR PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.

KW Complete proteome.

SQ SEQUENCE 257 AA; 29674 WW; 56B0A6D952EDFED4 CRC64;
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PubMed=15213324; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Bright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.,
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus (strain MRSA252).
Bacteria; Firmicutes; Bacillales; Staphylococcus
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82.0%; Pred. No. 3.5e-76;
bive 17; Mismatches 25
                                                                                                                                            81.8%;
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InterPro; IPR006177; Bctr tox.
InterPro; IPR006177; Bctr tox.
InterPro; IPR006173; Stap/Strept tox.
InterPro; IPR006136; Staph/Strept tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxIN.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 260 AA; 29708 MW; 087C5B4EC0280
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01-JUN-2001
01-JUN-2001
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Lancet 357:1225-1240(2001).
EMBL; AP003135; BAB43036.1; -.
EIREL; AP003135; BAB43036.1; -.
EIR; C89984; C89984.
HSSP; P13163; 1SXT.
G0; G0:0005576; C:extracellular; IEA.
G0; G0:0005576; P:pathogenesis; IEA.
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llarity 79.0%; Pred. No. 8.5e-74;
Conservative 17; Mismatches 32;
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Bacillales; Staphylococcus
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Enterotoxin J.
Name=sej;
Staphylococcus aureus.
Bacteria; Firmicutes; B
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Enterotoxin sea variant (Fragment).
Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
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219 AA;
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25264 MW; DE8E38AEB652FC89 CRC64;
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    Bacillales; Staphylococcus
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R GO; GO:0005576; C:excracellular; IEA.
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R InterPro; IPR006197; Bact endotox.
R InterPro; IPR006173; Bact endotox.
R InterPro; IPR006123; Stap/Strep_toxin.
R InterPro; IPR006123; Stap/Strept tox.
R InterPro; IPR006126; Staph/Strept tox.
R InterPro; IPR006173; Staph/Strept tox.
R InterPro; IPR006173; Staph/Strept tox.
R Ffam; PF01123; Stap Strp toxin; 1.
R Pfam; PF02876; Stap_Strp_tox_C; 1.
R Pfam; PF02876; Stap_Strp_tox_C; 1.
R PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
R PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
R PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
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R HSSP; P13163; IESF.

R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005976; P:pathogenesis; IEA.
R InterPro; IPR006177; Bctrl tox.
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R InterPro; IPR006173; Staph/Strept tox.
R InterPro; IPR006173; Staph/Strept tox.
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Bacteria; Firmicutes;
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HSSP; P13380; IAN8.
GO; GO:000575; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006992; Bact endotox.
InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006123; Staph_tox_OB.
Pfam; PF0123; Stap Strp_toxin; 1.
Pfam; PF02876; Stap Strp_toxin; 1.
PROSITE; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREE_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREE_TOXIN_2; 1.
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PROSITE; PS00277; STAPH STREP TOXIN_1;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Simultaneous analysis of multiple staphylococcal enterotoxin an oligonucleotide microarray assay.";
J. Clin. Microbiol. 42:2134-2143/^^^^
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InterPro; IPR006177; BctrI tox.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006133; Staph tox OB.
Pfam; PF01123; Stap_Strp_tox(OB.
Pfam; PF01123; Stap_Strp_toxIn; 1.
PRNOTS; PR00279; BACTRITOXIN.
PRNOTS; PR00279; BACTRITOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89359112; PubMed-2549000;
Bayles K.W., Iandolo J.J.;
"Genetic and molecular analyses of the gene encoding staphylococcal
                                                                                                                                                                                                                                                                                                                                   EMBL; M28521; AAB0619
PIR; A33953; A33953.
                                                                                                           PROSITE; PS00277; STAPH STREP TOXIN 1; PROSITE; PS00278; STAPH STREP TOXIN 2; Enterotoxin; Signal; Superantigen; Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 23235;
MEDLINE=97157473; PubMed=9003758;
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"The crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer; zinc-dependent.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Staphylococcal enterotoxins cause staphylococcal food poisoning syndrome. The by high fever, hypotension, diarrhea, shock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crystal structure of staphylococcal enterotoxin
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(Rel. 44,
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR00892; Bact endotox.
InterPro; IPR008177; BctrI tox.
InterPro; IPR006127; BctrI tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox_OB.
InterPro; IPR006173; Staph tox_OB.
Pfam; PF01123; Stap Strp_tox_C; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.
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SEQUENCE
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EMBL; AY518388; AAR99636.1; -.
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                                                                                                            1 FKSKNVDVYAIRYSINCYGGEIDRTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVS
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DAQGQYPDTLLRIYRDNKTINSENLHIDLYLY
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Pred. No. 1.6e-46;
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR00892; Bact endotox.
InterPro; IPR008177; BctrI tox.
InterPro; IPR008127; BctrI tox.
InterPro; IPR008128; Staph/Strept toxin.
InterPro; IPR008128; Staph_tox_OB.
InterPro; IPR008128; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; UN
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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HSSP; P13163; 1SXT.
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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OrderedLocusNames=SAS1538;
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| DVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLY
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                                         (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
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RAX Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Dogett J., Dowd L.,
RA Peltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL, BX571857; CAG43339.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR006173; Bctrl tox
DR InterPro; IPR006173; Staph tox OB.
DR InterPro; IPR006173; Staph tox OB.
DR InterPro; IPR006173; Staph tox OB.
DR Ffam; PF01123; Stap Strp toxin.
DR Pfam; PF02876; Stap Strp toxin.
DR Pfam; PF02876; Stap Strp toxin; 1.
DR Pfam; PF02876; Stap Strp Tox.C: 1.
DR PROSITE; PS00279; STAPH_STREP_TOXIN_1; UNKNOWN 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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Matches 91
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Q7A2Q6;
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
                                                                                                                                                                         Staphylococcus aureus
Bacteria; Firmicutes;
NCBI_TaxID=158878;
                                                                                                                                                                                                                                           Name=sen; OrderedLocusNames=SAV1825; Staphylococcus aureus (strain Mu50 /
                                                                                                                                                                                                                                                                                                      Enterotoxin.
                                                                                                                       SEQUENCE FROM N.A.
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bcttl tox.
InterPro; IPR006177; Bcttl tox.
InterPro; IPR006123; Stap/Strept_tox.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006123; Staph tox OB.
Pfam; PF01123; Stap Strp_toxin; I.
Pfam; PF01237; Stap Strp_tox C; 1.
PRINTS; PR00279; BACTRITOXIN.
PRINTS; PR00279; BACTRITOXIN.
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Q7A4X1;
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05-UUL-2004 (TrEMBLrel. 2:
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                                                                                                                                   Hattori M., Og
"Whole genome
aureus.";
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MEDLINB=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
Lancet 357:1225-1240(2001).

EMBL; AP003135; BAB42911.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008992; Bact_endotox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=sen; OrderedLocusNames=SA1643;
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus
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PROSITE; PS00278; STAPH_STREP_TOXIN_2;
Complete proteome,
SEQUENCE 258 AA; 29676 MW; BA6C0741
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InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006126; Staph tox OB.
Pfam; PF0123; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp toxin; 1.
PRINTS; PF00279; BACTRUTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 258 AA; 29676 MW; 8A6C074F3E
                                                                     HSSP; 053588; 1877.

GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/strept_tox.
InterPro; IPR006123; Staph_tox_OB.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF0123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRNOSITE; PS00279; BACTRUTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F8
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Q9EZM4;
01-MAR-2001
01-MAR-2001
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Staphylococcus aureus.
Bacteria; Firmicutes;
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MEDLINE-20571956; PubMed-11123352;
Lim A., Tristan A.,
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3 (TrEMBLrel. 25,
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J. Appl. Microbiol. 95:38-43(2003).

EMBL; AY158703; AA017733.1; -.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0005576; C:extracellular; IEA.

InterPro; IPR006577; Betri tox.

InterPro; IPR006123; Stap/Strep_toxin.

R InterPro; IPR006123; Staph/Strep_tox.

R InterPro; IPR006123; Staph/Strep_tox.

R InterPro; IPR006123; Staph/Strep_tox.

R InterPro; IPR006123; Staph/Strep_tox.

R InterPro; IPR006123; Staph/Strep_tox.

R InterPro; IPR006173; Staph/Strep_tox.

R Pfam; PF01123; Stap Strp_toxin; 1.

R Pfam; PF02876; Stap_Strp_tox_C; 1.

R PfANTS; PR00279; STAPH_STREP_TOXIN_1; UNKNOWN_1.

R PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC6
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Best Local :
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Letertre C., Perelle S., Dilasser F., Fach P.;
"Identification of a new putative enterotoxin SEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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9; Mismatches 77
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Staphylococcus aureus (strain MRSA252)
Bacteria; Firmicutes; Bacillales; Stap
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RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Foil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Ra Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
Ames K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
RRA Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl Acad. Sci. U.S.A. 101:9786-9791(2004).
RRA DRA CO. (20009405; P:pathogenesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006126; Staph/Strepttox:
RI InterPro; IPR006127; Staph/Strepttox:
RI InterPro; IPR006127; Staph tox OB.
RI InterPro; IPR006127; Staph tox OB.
RI InterPro; IPR006127; Staph tox OB.
RI InterPro; IPR006127; Staph tox OB.
RRA PROSITE; P800279; BACTRLTOXIN_
DR PRINTS; PR00279; BACTRLTOXIN_
DR PRINTS; P800279; BACTRLTOXIN_
DR PRINTS; P800279; BACTRLTOXIN_
DR PRINTS; P800279; BACTRLTOXIN_
DR PROSITE; P800279; STAPH STREP_TOXIN_1; UNKNOWN_1.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC64;
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RA Bright M.C., Foster T.J., Moore C.E., Hurst L., Akkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Dogett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT evidence for the rapid evolution of virulence and drug resistance.";
RR GO; GO:0005576; C:extracellular; IEA.
DR RMLL, BX571856; CA4409071; -.
DR RMLL, BX571856; CA4409071; -.
DR RMLL, BX571856; CA4409071; -.
DR RMC, SCO:0005405; P:pathogenesis; IEA.
DR InterPro; IPR006173; Staph/Strept_tox.
DR InterPro; IPR006173; Staph/Strept_tox.
DR InterPro; IPR006173; Staph/Strept_tox.
DR InterPro; IPR006173; Staph/Strept_tox.
DR Pfam; PF02183; Stap Strp_tox.C; 1.
DR Pfam; PF02187; Stap Strp_tox.C; 1.
DR Pfam; PF02173; STAPH_STREP_TOXIN_1; 1.
DR Pfam; PF0277; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
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99; Conser
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larity 40.9%; Pred. No. 5.1e-26;
Conservative 39; Mismatches 84
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Feil E.U., Lindsay J.A., Peacock S.J., Day
Foster T.J., Moore C.E., Hurst L., Atkin R.,
ley S.D., Chillingworth C., Chillingworth T.
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Staphylococcus aureus (strain N315).
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G0; G0:0009576; C:extracellular; IEA.
G0; G0:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR008177; Bctrī tox.
InterPro; IPR008123; Stap/Strept toxin.
InterPro; IPR008123; Staph/Strept tox.
InterPro; IPR008173; Staph tox_B.
Pfam; PF01123; Stap Strp_toxin; 1.
Pfam; PF02876; Stap Strp_toxin; 1.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
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EMBL; AP003363; BAB57992.1; -.
PIR; E89969; E89969.
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EMBL; AP003135; BAB42916.1; -.

GO; GO:0005576; C:extracellular; IRA.

GO; GO:0005576; C:extracellular; IRA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR006992; Bact_endotox.

InterPro; IPR006177; BctrI_tox.

InterPro; IPR006177; Stap/Strept_toxin.

InterPro; IPR006173; Stap/Strept_tox.

InterPro; IPR006173; Staph/strept_tox.

InterPro; IPR006173; Staph tox OB.

Pfam; PF01123; Stap Strp_toxin; 1.

PRINTS; PR00279; BACTRLTOXIN.

PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                       Q9EZM8;
Q9EZM8;
01-MAR-2001
01-MAR-2001
01-OCT-2003
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                                                   STRAIN=A900322;

MEDLINB=20571956; PubMed=11123352;

Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M.,

Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M.,

Etienne J., Vandenesch F., Bonneville M., Lina G.;

"egc, a highly prevalent operon of enterotoxin gene,
nursery of superantigens in Staphylococcus aureus.";

J. Immunol. 166:669-677(2001).
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PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                             Staphylococcus aureus. Bacteria; Firmicutes;
    EMBL; AF285760; AAG36951.1;
HSSP; Q54971; 1BXT.
GO; GO:0005576; C:extracell
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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      GO:0005576; C:extracellular;
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InterPro; IPR008992; Bact endoxox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006173; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF0123; Stap_Strp_tox_C; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 261 AA; 29949 MW; 24DA4DDD76
Query Match
                                                                GO; GO:000576; C:extracellular; IEA.
GO; GO:000576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF01237; Stap_Strp_tox: 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1
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Q52075;
01-NOV-1996
01-NOV-1996
01-OCT-2003
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Plasmid pIB485.
Plasmid pIB485.
other sequences;
                                                     PROSITE; Plasmid.
                                                                                                                                                                                                                              J. Bacteriol. 171:4799-4806 (1989)
EMBL; M94872; AAA98133.1; -.
HSSP; P13163; ISXT.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89359112; PubMed=2549000;
Bayles K.W., Iandolo J.J.;
"Genetic and molecular analyses of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterotoxin D.
                                   SEQUENCE
                                                                                                                                                                                                                                                                                      enterotoxin D.";
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| LFT 261
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                                     179 AA;
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; Pred. No. 8.1e
31; Mismatches
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     Score 381;
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     Length 179;
                                        CRC64;
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strep toxin.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp tox C; 1.
PRINTS; PR00279; BACTRLTOXIN.
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01-JUN-2002
01-OCT-2003
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.; "Detection of seg, seh, and sei genes in Staphylococcus aureus isolates and determination of the enterotoxin productivities of S aureus isolates Harboring seg, seh, or sei genes.";
J. Clin. Microbiol. 40:857-862(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=21871379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                       PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1280;
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170
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85; Conserv
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                                                                         WIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSS 189
                                                                                                    KFATADLAQKFKNKNVDIYGASFYYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV
                                                                                                                           DLGSKDATNKYKGKKVDLYGAYYGYQCAGGTENKTACMYGGVTLHDNNRLTEEKKVPINL 129
                                                                                                                                                                             KDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERKKIPINLWINGVQKEVSLDKVQTDKKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKKVPINLWIDGKQTTVPIDKVKTSKKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NENIDSVKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDQFLENTLLYKKFFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTG
TPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT
                        EGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENL-HIDLYLYT
                                                 WVDGIOKETEL
                                                                                                                                                       EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV
                                                                                                                                                                                                                                                          217
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2 (TrEMBLrel. 21,
3 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11880405;
                                                                                                                                                                                                                                                          25143 MW; A8A44E23F31DE80D CRC64;
                                                                                                                                                                                                                   29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales; Staphylococcus
                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                Score 366; DB 2;
Pred. No. 3.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.8e-23;
4; Mismatches 53;
                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                       81;
                                                                                                                                                                                                                             Length 217;
                                                                                                                                                                                                        Indels
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213
                      232
                                                  EISKGLIEFDMK
                                                                                                                                                                                                       12;
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                                                  169
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RESULT

26

FALSE_NEG

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pDB; 1EWC; X-ray; A=26-337.

pDB; 1EWC; X-ray; A=26-339.

pDB; 1F7; X-ray; A=26-337.

pDB; 1F7; X-ray; D=25-31.

pDB; 1F7; X-ray; D=25-37.

InterPro; IPR006177; BctrI tox.

InterPro; IPR006173; Stap/Strep_toxin.

InterPro; IPR006173; Stap/Strep_tox.

InterPro; IPR006173; Staph/Strept_tox.

InterPro; IPR006173; Staph/Strept_tox.

InterPro; IPR006173; Staph_Strp_tox_OB.

pfam; pF0123; Stap_Strp_toxIn; 1.

pfam; pF0123; Stap_Strp_toxIn; 1.

pROSITE; pS00279; STAPH_STREP_TOXIN_2; 1.

pROSITE; pS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETXH STAAW
Q53585;
29-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).

Y-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).

PubMed=10986116; DOI=10.1006/jmbi.2000.4093;

Hakekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,

Antonsson P., Svensson L.A.;

"The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TcR molecules.";

J. Mol. Biol. 302:527-537(2000).

-1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterotoxin type H precursor (SEH).
Name=entH; Synonyms=seh; OrderedLocusNames=MW0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren K., Bannan J.D., Pancholi V
Fischetti V.A., Zabriskie J.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=D4508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain MW2),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization and biological properties of a new staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necess for the toxin interaction with MHC class II. SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin.
                                                                                                                                                                                                                                                                 U11702; AAA19777.1;
                                                                                                                                                                                                                                               AP004822; BAB93916.1; -.
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(Rel. 43,
(Rel. 45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7964453;
                                                                                                                                                                                                                                                                                                                  institutions as long as its content is atement is not removed. Usage by and for license agreement (See http://www.isb-sib.
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Query Match
Best Local Similarity
Matches 85; Conserv
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EMBL; AY345144; AAQ63188.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bactl tox
InterPro; IPR006173; Stap/Strep_toxin.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap Strp_toxin; 11.
Pfam; PF02876; Stap Strp_tox C; 1.
PRINTS; PR00279; BACTRITOXIN.
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Q6VAM8;
05-JUL-2004 (TremBLrel. 2
05-JUL-2004 (TremBLrel. 2
05-JUL-2004 (TremBLrel. 2
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SIGNAL
SIGNAL
CHAIN
METAL
DISULFID
SEQUENCE
24
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Staphylococcus aureus.
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                                                                                        CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FRI 137;
Gul'ko L.B., Voyushi
Veiko V.P., Debabov
                                                                                                                                   PROSITE; PS00278;
Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The Obtaining of the Tumor-Addressed Genetically Engineered Drug Cancer Immunotherapy. II. Cloning a Gene of the pro-Enteroxin H (cancer Immunotherapy and the Expression in Escherichia coli. From Staphylococcus aureus, its Expression in Escherichia coli. Investigation of the Enterotoxin H Secretion by E. coli Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1280;
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241 AA;
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241 AA;
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voyushin K.E., Fluer F.S., Debabov V.G.;
                                                                                                                                                                                 STAPH_STREP_TOXIN_2;
                                                                                        241 e
27831 MW;
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                     29.6%; Score 366; DB 2; 37.9%; Pred. No. 4.3e-22;
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Last annotation update)
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                                                                                           enterotoxin H.; 70EBA8418C9ECCFE CRC64;
                                                                                                                                      Potential.
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  81;
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                                           Length 241;
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Ax Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Ax Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Ax Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Ax Churcher C., Clark L., Corton C., Cronin A., Dogett J., Dowd L.,
Ax Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
Ax James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ax Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Sanders M.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ax Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
BY T. Complete genomes of two clinical Staphylococcus aureus strains:

Ax Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

BY TOO Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

BY TOO Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

BY TOO Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

BY GO; GO:0005576; C:extracellular; IEA.
BY GO; GO:0005576; C:extracellular; IEA.
BY GO; GO:0005576; C:extracellular; IEA.
BY GO; GO:0005576; C:extracellular; IEA.
BY GO; GO:000577; Staph tox OB.

BY TOO NATL ACAD. Staph Strap Loxin.

BY TOO NATL ACAD. Staph Strap Loxin.

BY TOO NATL ACAD. Staph Strap Loxin.
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Best Local Similarity
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-seh; OrderedLocusNames=SAS0051;
Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 241 AA;
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TPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT
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                                  WIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSS
                                                                                                              DLGSKDATNKYKGKKYDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINL 129
                                                                                                                                                                                          KDLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                            KFATADLAQKFKNKNVDIYGASFYYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV
                                                                                                                                                        EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV
  WVDGIOKETEL--IRTNKKNVTLOELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 193
                                                                                                                                                                                                                                                                                                                  241 AA;
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                  27858 MW; 70F77985877616CE CRC64;
                                                                                                                                                                                                                                                      29.6%; Score 366; DB 2; 37.9%; Pred. No. 4.3e-22;
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Last annotation update)
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Best Local :
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                             Q6GFM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22692404; PubMed=12807452; Letertre C., Perelle S., Dilasser F., Fach P., "Identification of a new putative enterotoxin cluster of Staphylococcus aureus."; J. Appl. Microbiol. 95:38-43(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus. Bacteria; Firmicutes;
                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strp_toxin; 1.
Pfam; PP01123; Stap_Strp_toxin; 1.
Pfam; PP02876; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                   Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                     OrderedLocusNames=SAR1919;
                                                                                                                                               Enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; IEA.
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SEQUENCE
                                         NCBI_TaxID=282458;
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P13380; IAN8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIKDL---SYAQGDIGVGNLRNFYTKYDYIDLKGVTDKNLPIANQLE-----FSTG--
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TPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT
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4 (TrEMBLrel. 27,
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1 N.A.
                                                                                             aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%; Score 348.5; DB 2; 36.6%; Pred. No. 1.2e-20; tive 37; Mismatches 77;
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RA Holden M.T.G., Feile E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Feile E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Holden M.T.G., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RR Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RMBL; BX571856; Chad40905.1; -
DR GO; GO:0009405; P:pathogenesis; IEA.
CO, GO:0009405; P:pathogenesis; IEA.
RR GO; GO:0009405; P:pathogenesis; IEA.
RR GO; GO:0009405; P:pathogenesis; IEA.
RR InterPro; IPR006127; Bctrl tox.
RR InterPro; IPR006127; Bctrl tox.
RR InterPro; IPR006127; Sctaph_tox_CB
RR InterPro; IPR006123; Stap/Strep_toxin.
RR Ffam; PP01213; Stap_Strp_tox_C; 1.
RR Ffam; PF02876; Stap_Strp_tox_C; 1.
RR Ffam; PR0279; BACTRLTOXIN.
RR Complete proteome.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;
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Q8VVW1;
01-MAR-2002
01-MAR-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                     NCBI_5
EMBL; AF438524; AAL31571.1;
HSSP; P13163; 1SXT.
GO; GO:0005576; C:extracell
                                                                                                                                     MEDLINE=21259899; PubMed=11359827;
Proft T., Arcus V.L., Handley V., Baker E.N., Frase
"Immunological and biochemical Characterization of
pyrogenic exotoxins I and J (SPE-I and SPE-J) from
                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exotoxin
                                                                                     pyogenes.";
J. Immunol.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                     166:6711-6719(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SYAQGDIGVGNLKNFYTKYDYIDLKGVTDKNLPIANQLE----FSTG--
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Last sequence up
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Best Local S
Matches 77
                  PIR; C89969; C89969.

HSSP, P13380; IKTK.
G0; G0:0005576; C:extracellular; IEA.
G0; G0:0005576; C:extracellular; IEA.
G0; G0:0005405; P:pathogenesis; IEA.
InterPro; IPR008192; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strep_toxin; 1.
Pfam; PF012876; Stap/Strp_tox_C; 1.
Pfam; PF02876; Stap/Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSTIE; PS00278; STAPH_STREP_TOXIN_2; 1
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O85383;
01-NOV-1998
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Pfam; PF012376; Stap_Strp_tox_C; 1.
PR.NITS; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH_STREEP_TOXIN_1; UNKNOWN_1.
PROSITE; PS00278; STAPH_STREEP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREEP_TOXIN_2; 1.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Etienne J., Vandenesch F., Bonneville M., Lina G.; "egc, a highly prevalent operon of enterotoxin gene, nursery of superantigens in Staphylococcus aureus."; J. Immunol. 166:669-677(2001).
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                     STAPH_STREP_TOXIN_2;
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34.8%; Pred. No. 4.2e-20;
tive 42; Mismatches 79
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CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21311952; PubMed-11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
                                                                                                                                                     Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLITOXIN.
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
Complete proteome.
SEQUENCE 242 AA; 27863 MW; C5C8B4AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                          EMBL; AP003363; BAB57990.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogeneais; IEA.
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Name=sei; OrderedLocusNames5AV1828;
Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                            InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006173; Staph tox OB.
                                                                                                                                                                                                                                                                                                                                                                       "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
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                                                             LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN
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   KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBKKVPINLWIDGKQTTV
                                VGNLRNFYTKHDYIDLKGVTDKNLPIANQLB-----FSTG---TNDLISESNNWDEIS
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25
242 AA;
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242 e
27863 MW;
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                                                                                                           35.6%;
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; C5C8B4ACEE5414A8 CRC64;
                                                                                                           Score 339.5; DB 2
Pred. No. 6.7e-20;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Stap/Strep toxin.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp tox O:
PRINTS; PR00279; BACTRITOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7A4W8

Q7A4W8, PRELIMINARY;

Q5-JUL-2004 (TrEMBLrel. 27,

Q5-JUL-2004 (TrEMBLrel. 27,

Q5-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome sequencing of aureus.";
Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular enterotoxin type I. Name=sei; OrderedLocusNames=SA1646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                       VGNLRNFYTKHDYIDLKGVTDKNLPIANQLE-----FSTG---TNDLISESNNWDEIS
                                                                                                                                                                                                                                                                                                                                                                 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN
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                                                             HLNNEKSFSYDLFYTGDGLPVSFLKIYEDNKIIESEKFHLDV
                                                                                                     HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                   KFKGKKLDIFGIDYNGPC-----KSKYMYGGATL-SGQYLNSARKIPINLWVNGKHKTI 132
                                                                                                                                                                                                                                                                           KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV 138
                                                                                                                                                                                                                                                                                                                                                                                                           27.4%;
llarity 35.6%;
Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27863 MW; C5C8B4ACEE5414A8 CRC64;
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Pred. No. 6.7e-20;
6; Mismatches 74;
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~hes 74; Indels
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RESULT 36
Q7A4W
ID Q7A4W
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AC Q7A4W
DT 05-JU
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                                       Extracellular enterotoxin L.
Name=sel; OrderedLocusNames=SA1816;
                      Staphylococcus aureus (strain N315)
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RESULT 35

Firmicutes;

Bacillales; Staphylococcus

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Matches
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EMBL; AP003364; BAB58170.1; -.

HSSP; P13380; 1AN8.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR006177; Bctr1 tox.

InterPro; IPR006177; Bctr1 tox.

InterPro; IPR006133; Stap/Strept_toxin.

InterPro; IPR006133; Staph/Strept_tox.

InterPro; IPR006135; Staph/Strept_tox.

InterPro; IPR006137; Staph/Strept_tox.

PRINTS; Stap Strp_tox. OB.

PRINTS; PR00279; BACTRITOXIN.

PRINTS; PR00279; BACTRITOXIN.
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Q7A2N9;
05-JUL-2004 (TrEMBLrel. 27, Cr
05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
Extracellular enterotoxin L.
Q7A4K9 PRELIMINARY; PRT; 240 AA.
Q7A4K9
Q7A4K9
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=sel; OrderedLocusNames=SAV2008;
Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
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                                                                                                                                                                                                                                                                         195 MNDGSNFSYDLFYTGYGLPESFLKIYKDNKTVDSTQFHLDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 YKGKKVDLYGAYYGYQCAGGTPNKTACMYGGYTLHDNNRLTEEKKVPINLWIDGKQTTVP 139
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                                                                                                                                                                                                                                                                                                                                           SSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                       TKSVSTDKKMVTAQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSSKFYSGFDKGSVVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDKVKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LLVDLGSKDATNK 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 337; DB 2; Length 240; 35.3%; Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
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Last sequence update)
Last annotation updat
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RESULT 37
Q9F0L7
ID 09F0L
AC Q9F0L
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M2
ES1.
GN Name
OS Stap
OC Bact
OX NCB1
RN (1)
RP SEQ!
RA Fit
RA Mea
RT "C'
RT J.
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InterPro; IPR008992; Bact endotox.
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InterPro; IPR006133; Stap/Strep toxin.
InterPro; IPR006133; Stap/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006137; Staph tox OB.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF01237; Stap Strp toxin; 1.
PRINTS; PR00279; BACTRITOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                                          Q9F0L7;
01-MAR-2001
01-MAR-2001
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EMBL; AP003135; BAB43096.1;
HSSP; P13380; LAN8
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MEDLINE=2056668; PubMed=11114901; DOI=10.1128/JB.183.1.63

Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Ha

Meaney W.J., Smyth C.J.;

"Characterization of a putative pathogenicity island from

Staphylococcus aureus encoding multiple superantigens.";

J. Bacteriol, 183:63-70(2001).
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tive 37; Mismatches 72
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R GO; GO:0005405; P:pathogenesis; IEA.
R InterPro; IPR008992; Bact endotox.
R InterPro; IPR006173; Bact tox.
R InterPro; IPR006123; Stap/Strep toxin.
R InterPro; IPR006126; Staph/Strept tox.
R InterPro; IPR006173; Staph tox_OB.
R InterPro; IPR006173; Staph tox_OB.
R Pfam; PF01123; Stap Strp toxin; 1.
R Pfam; PF02876; Stap Strp toxin; 1.
R PRNNTS; RR00279; BACTRITOXIN.
R PRNNTS; PS00279; BACTRITOXIN.
R PROSITE; PS00279; STAPH_STREP_TOXIN_1; UNKNOWN_1.
R PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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GO; GO:0005405; P:pathogenesis; IEA.
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InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_tox.
InterPro; IPR00613; Staph_tox_OB.

Pfam; PF01123; Stap_strp_toxin; 1.
Pfam; PF02876; Stap_strp_toxin; 1.
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Extracellular enterotoxin L.
Name=sell; OrderedLocusNames=MW0760;
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
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HSSP; Q9RQQ5; 1ET6.
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"Genome and virulence determinants
acquired MRSA.";
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Last sequence update)
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GO; GO:000576; C:extracellular; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_tox_C; 1.
Pfam; PF02876; Stap_Strp_tox(C; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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SEQUENCE
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Staphylococcus aureus
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01-JUN-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus isolates Harboring seg, seh, or sei
J. Clin. Microbiol. 40:857-862(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21871379; PubMed=11880405;
Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa
"Detection of seg, seh, and sei genes in Staphylococcus aureus
isolates and determination of the enterotoxin productivities o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterotoxin I (Fragment)
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240 AA;
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                                                      PIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQRGLIVF
                                                                                                                                  KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV
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                  STDKIATNKKLYTAQEIDVKLRRYLQEEYNIYGHNNTGKGKEYGYKSKFYSGFNNGKVLF
                                                                                              KFKGKKLDIFGIDYNGPC----
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ilarity 35.3%;
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35.1%; Pred. No. 1.36
tive 37; Mismatches
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Pred. No. 1.3e
37; Mismatches
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.3e-19;
72;
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                                                                                                                                                                                                                                                                                       Length 218;
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Matches 76
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GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR006197; Bact_ tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF0123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PFANNTS; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                              Q99ZZ1;
Q99ZZ1;
01-JUN-2001
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Q9L921;
Q1-Q2T-2000 (TrEMBLrel. 15,
01-QCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                    Streptococcal exotoxin I. Name=speI; OrderedLocusNames=SPy1007;
                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SePB-I of Streptococcus equi.";
Microb. Pathog. 32:71-85(2002).
EMBL, AF186180; AAF72808.1; -.
HSSP; P13163; 1SXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21671707; PubMed=11812213; DOI=10.1006/mpat.2001.0482; Artiushin S.C., Timoney J.F., Sheoran A.S., Muthupalani S.K.; "Characterization and immunogenicity of pyrogenic mitogens SeP
                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artiushin S.C., Timoney J.F., Sheorar "Characterization and immunogenicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDG----KQTTV 138
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                                                                                                                                                                                                                                                                                                                                                      PIDKVKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGKVQRGLIVFHSS 189
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  Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                         PRELIMINARY;
                pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.1%; Score 335.5; DB 2 34.4%; Pred. No. 1.3e-19; tive 42; Mismatches 80
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  Lactobacillales;
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  Streptococcaceae;
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Best Local S
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GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Betri tox.
InterPro; IPR006123; Stap/Strept_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap Strp_toxin; 1.
Pfam; PF012876; Stap Strp_tox C; 1.
PRINTS; PR00279; BACTRITOXIN.
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Q99T47;
01-JUN-2001
01-JUN-2001
01-OCT-2003
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MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
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SEQUENCE FROM N.A.

STRAIN-MUSO / ATCC 700699;

MEDLINE-21311952; PubMedell1418146; DOI=10.1016/80140-6736(00)04403-2;

KURODA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Mizutani-Ui Y., Takahashi N.K., Sawano S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                            Name-sem; OrderedLocusNames=SAV1829;
Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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NCBI_TaxID=1314;
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GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR008177; Bctr1 tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006173; Stap tox OB.
Pfam; PF01123; Stap_Strp_tox C; 1.
Pfam; PF02876; Stap_Strp_tox C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
                           "Whole genome sequencing of meticillin aureus.";
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EMBL; AP003135; BAB42915.1; ---
HSSP; P13380; 1AN8.
GO; GO:00095576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008197; Bctrl tox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006177; Stap/Strep toxin.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CVI I., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

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Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

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Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
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05-JUL-2004
05-JUL-2004
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Q7A4W7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP003363; BAB57991.1;
PIR; D89969; D89969.
HSSP; Q9RQQ5; IET6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=sem; OrderedLocusNames=SA1647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterotoxin SEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLMIDGKQTTVPIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAVDVYGLSYSGYCL----KNKYIYGGVTL-AGDYLEKSRRIPINLWVNGEHQTISTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLRN--YYGSYPIEDHQSINPENNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLROIYYYNEKAITENK--ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSTVSYDLFDAQGQYPDTLLRIYRDNKTINSBNLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSSGFNAGKILFHLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSFSYDLFDTGTGQAESFLKIYNDNKTVETEKFHLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKTSKKEVTVQELDLQARHYLHGKFGLY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
; Bctrl tox.; Stap/Strep toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%; Score 320; DE 33.0%; Pred. No. 2.76 tive 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (strain N31:
Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27,
27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5F29665125705600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NSDSFGGKVQRGLIVFHSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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 Best Loc
Matches
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Best Local
                          Query
                                                                                                           GO; GO:00055/6; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bcctrl tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_tox.
InterPro; IPR006126; Staph_exotoxin.
InterPro; IPR008175; Staph_exotoxin.
InterPro; IPR008175; Staph_exotoxin.
InterPro; IPR006173; Staph_tox.OB.
Pfam; PF01276; Stap_Strp_tox.C; 1.
Pfam; PF0276; Stap_Strp_tox.C; 1.
PRINTS; PR01800; STAPHEXOTOXN.
PRINTS; PR01800; STAPHEXOTOXN.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Cre
01-OCT-2002 (TrEMBLrel. 22, Las
01-MAR-2004 (TrEMBLrel. 26, Las
staphylococcal enterotoxin SeG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                    PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 242 AA; 28139 MW; FFCC89BB0E7A3BF5 C
                                                                                                                                                                                                                                                                                       Lancet 359:1819-1827(2002).
EMBL; AP004828; BAB95802.1; -.
HSSP; P13380; 1KTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8NVM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 239 AA; 27370 MW; SE29665125705600 CRC64;
                                                                                                                                                                                                                                                                                                                                   acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=seg2; OrderedLocusNames=MW1937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBNVM3;
             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
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              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQTTVPIDK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFHSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAVDVYGLSYSGYCL-----KNKYIYGGVTL-AGDYLEKSRRIPINLWVNGEHQTISTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSFSYDLFDTGTGQAESFLKIYNDNKTVETEKFHLDV 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSSGFNAGKILFHLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLRN--YYGSYPIEDHQSINPENNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLRQIYYYNEKAITENK--ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.8%; Score 320; DB
33.0%; Pred. No. 2.7e
Live 40; Mismatches
             25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (strain MW2).
Bacillales; Staphylococcus
  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Score 319.5; DB
Pred. No. 3e-18;
5; Mismatches
                                                        FFCC89BB0E7A3BF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
  71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
  Indels
                             242;
 43;
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 Gape
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RESULT 45
QGGTUI

ID QGGTUI

AC QGGTU

DT Q5-JT

DT Q5-JT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCOmplete genomes of two clinical Staphylococcus aureus strains:

re evidence for the rapid evolution of virulence and drug resistance.";

Remot. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; -.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

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REMBL; BX571857; CAG43727.1; LEA.

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REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

REMBL; BX571857; CAG43727.1; LEA.

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REMBL; BX571857; LEA.

REMBL; BX571857; 
                                                                                                                                                                                                                                                                                  Matches
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Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Barright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
"Formaler's Conserved."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6G7U1;
Q6G7U1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterotoxin.
OrderedLocusNames=SAS1920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=282459;
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   77
                                                              81 KGK-----KVDLYGAYYGYQCAGGTENKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQ 135
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                            proteome.
242 AA; 28139 MW; FFCC89BB0E7A3BF5 CRC64;
                                                                                                                                       NLRNFYANYQPEKLQGVSSGNFSTSHQLE---YIDGKYTLYSQFH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGK-----KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQ 135
                                                                                                                                                                                                         NLRQIY --YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTISTOKVSTOKKEVTAQEIDIKLRKYLQNEYNIYGFNKTKKGQEYGYKSKFNSGFNKGK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKRIKDHKVDIFGISYSGIC-----NTKYMYGGITLANQN-LDKPRNIPINLWVNGKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL
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(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                               25.8%; Score 319.5; DE 33.8%; Pred. No. 3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain MSSA476)
Bacillales; Stap
                                                                                                                                                                                                                                                                                  35;
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                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                  71;
                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                  Indels
   |-LDKPRNIPINLWVNGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
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                                                                                                                                              ----NEY
                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                  Gaps
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       129
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RESULT
Q8VLW7
  RESULT
Q93CC6
ID Q9
AC Q9
DT 01
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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01-MAR-2002
01-MAR-2002
Q93CC6;
Q93CC6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin.
PRINTS; PR00279; BACTRLTOXIN.
PRINTS; PR01800; STAPHEXOTOXIN.
PROSITE; PR000279; STAPH_STREEP_TOXIN_1; UNKNOWN_1.
PROSITE; PS000279; STAPH_STREEP_TOXIN_2; 1.
SEQUENCE 256 AA; 29794 MW; 9E2F13790823A7DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=9838524; PubMed=9720870;
Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Ro
"The gene for toxic shock toxin is carried by a fig
pathogenicity islands in Staphylococcus aureus.";
Mol. Microbiol. 29:527-543(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RN4282;
Barry P.C., Novick R.P.;
Submitted (JAN-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U93688; AAL67620.1;
HSSP; P13380; 1KTK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=entQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcal enterotoxin Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1280;
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                                                                                                                                                                                                                                                      NLRQIY -- YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITPHLNNEPSFTYDLFYTGTGQAESFLKIYNDNKTIDAENFHLDV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVFHSSEGSTVSYDLFDAQGQYFDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTISTDKVSTOKKEVTAQEIDIKLRKYLQNEYNIYGFNKTKKGQEYGYKSKFNSGFNKGK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN-----SDSFGGKVQRGL
                                                                                                                                                                                                                                  NTISTDKVSTQKKEVTAQEIDIKLRKYLQNEYNIYGFNKTKKGQEYGYQSKFNSGFNKGK
                                                                                                                                                                                                                                                                                                                                                              KGK-----KVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ
                                                                                                                                             IVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                      EAKRLKDHKVDIFGISYSGLC-----NTKYMYGGITLANQN-LDKPRNIPINLWVNGKQ
                                                                                                                                                                                                                                                                                                                                                                                                        NLRNFYANYEPEKLOGVSSGNFSTSHOLE---YIDGKYTLYSOFH------NEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  (TrEMBLrel.
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the
  19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
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  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 318.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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3.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
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GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctr1 tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006185; Staph_exotoxin.
InterPro; IPR008175; Staph_exotoxin.
InterPro; IPR006173; Staph_exotoxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF012876; Stap_Strp_tox_C; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR01800; STAPHEXOTOXN.
PRINTS; PR01800; STAPHEXOTOXN.
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PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

SEQUENCE 242 AA; 28184 MW; F6EEFD4AF8C30D85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF410775; AAL04146.1; HSSP; P13380; 1KTK.
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  MEDLINE=20571956; PubMed=11123352;
Jarraud S., Peyrat M.A., Lim A., Tristan
                                            SEQUENCE FROM N.A.
STRAIN=A900322;
                                                                                                                               Staphylococcus aureus. Bacteria; Firmicutes;
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Schlievert P.M.;
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MCCormick J.K., Paustian M.L., Orwin P.M., Kapur
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"egc, a highly prevalent operon of enterotoxin gene, form
nursery of superantigens in Staphylococcus aureus.";

J. Immunol. 166:669-677(2001).

R EMBL; AF285760; AAG36552.1; -.

R HSSP; Q9RQQ5; 1ET6.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR008992; Bact endotox.

R InterPro; IPR008992; Bact endotox.

R InterPro; IPR006177; Bctr] tox.

R InterPro; IPR006173; Stap/Strep toxin.

R InterPro; IPR006173; Stap/Strep toxin.

R Pfam; PF01123; Stap_Strp_tox.

R Pfam; PF02876; Stap_Strp_tox.

R Pfam; PF02876; Stap_Strp_tox.

R PRINTS; PR00279; BACTMINTOXIN.

R PROSITE; PS00278; STAPH_STREP_TOXIN.

PROSITE; PS00278; STAPH_STREP_TOXIN.

2 SEQUENCE 239 AA; 27371 MW; 69240B823C44028A CRC64;
                                                                                                                                                                                                                                                                     Becker K.;

Becker K.;

Thesis (2001), Department of Institute of Medical Microbiology, University of Muenater, Muenater, Germany.

EMBL; AJ307889; CAC86191.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR066123; Stap/Strep_toxin.

Pfam; PF02876; Stap Strp_tox C; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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                                                                                                                                                                                                                        SEQUENCE
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l Similarity 32.6%; Pred. No. 5.7e-18;
71; Conservative 41; Mismatches 78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKTSKKEVTVQELDLQARHYLHGKFGLY------NSDSFGGKVQRGLIVFHSSE 190
                           VNLWLHGKQTSVPLDTVRTYKKEVTVQELDLKARHYLHEKYNLYNPDAFGGKIQRGLIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSSFSYDLFDTGTGQAESFLKI YNDNKTVETEKFHLDV
                                                                                                                                                                                                                        86 AA;
                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intermedius
                                                                                                                                                                                                                        9877 MW;
                                                                                                                                              25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillales; Staphylococcus
                                                                                                                  Score 312; DB 2; Length 86; Pred. No. 3.5e-18; 5; Mismatches 14; Indels
                                                                                                                                                                                                                     21C191E65EAF72AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
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(Q8NVW)
1D Q9NVM
AC Q8NVM
AC Q8NVM
DT 01-QC
DT 01-QC
DT 01-QC
DT 01-QC
DT 01-QC
RESULT
QN Name;
QN Stap;
QN NAME;
QN NED;
RN [1]
RN [1]
RN [1]
RN [1]
RN [1]
RN HS(
RA Bab;
RA MED;
RA MED;
RA HS(
DR RT "Ge
RT "Ge
RT Lar
DR EME
DR HS(
DR GO
DR GO
DR GO
DR III
DR III
DR III
DR III
DR III
DR III
DR III
DR F;
DR GO
DR GO
DR GO
CKW C
SQ S
RESULT 51
Q6G7U0
ID Q6G7U
AC Q6G7U
DT 05-JU
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Best Local S
Matches 74
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EMBL; AP004028; BAB95803.1; -.

HSSP; P13380; IXTK.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

InterPro; IPR008192; Bact endotox.

InterPro; IPR006177; Bactri tox.

InterPro; IPR006173; Stap/Strep toxin.

InterPro; IPR006173; Stap/Strep toxin.

InterPro; IPR006173; Stap/Strep toxin.

Pfam; PF01123; Stap/Strp tox.C; 1.

Pfam; PF02876; Stap/Strp tox.C; 1.

PROSITE; PR00279; BACTRITOXIN.

COMPLETE PROCEOME.

COMPLETE PROCEOME.
                    Q6G7U0, PRELIMINARY;
Q6G7U0;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Enterotoxin.
OrderedLocusNames=SAS1921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8NVM2;
Q8NVM2;
01-OCT-2002
01-OCT-2002
Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Nagal Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., Termata of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcal enterotoxin Sek.
Name=sek2; OrderedLocusNames=MW1938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 NFKGKKLDVFGISYNGQC-----NTKYIYGGITA-TNEYLDKPRNIPINIWINGNHKTI 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         PIDKVKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VQRGLIVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDNLRNFYTKKDFINLKDVKDN----DTPIANQLQF----SNESY-DLISESKDFNKFS 78
                                                                                                                                                                                                                                                                                            HLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDV
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                                                                                                                                                                                                                                                                                                                                               HSSEGSTVSYDLF-DAQGQYPDTLLRIYRDNKTINSENLHIDL 228
                                                                                                                                                                                                                                                                                                                                                                                               STNKVSTNKKFVTAQEIDIKLRRYLQEEYNIYGHNGTKKGEEYGHKSKFYSGFNIGKVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;
                                                                    (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
aureus (strain MSSA476).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 310; DB 2; Length 242; 33.2%; Pred. No. 1.8e-17; Live 39; Mismatches 76; Indels
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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SO CC

Gaps

116

180

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Matches
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Best Local Similarity
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EMBL; BX571857; CA643728.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
Interpro; IPR008992; Bact endotox.
Interpro; IPR006177; BECTI tox.
Interpro; IPR006173; Stap/Strep toxin.
Interpro; IPR006173; Stap/Strep toxin.
PF01123; Stap Strp toxin; D.
PFINTS; PR00279; BACTRLYOXIN.
PRINTS; PR00279; BACTRLYOXIN.
"Simultaneous analysis of multiple staphylococcal an oligonuclectide microarray assay.";
J. Clin. Microbiol. 42:2134-2143(2004).
EMBL, AY518389; AAR99637.1; -.
HSSP; P13380; 1AN8.
                                                                                                                                                                                                                                                              Q6R2F8;
Q6R2F8;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lemard N., Line A., Mayes R., Moule S., Mungall K.,
James K.D., Lemard N., Line A., Mayes R., Moule S., Rungall K.,
Cronin D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Charles G., Cimmode M., Crowner W., Whitehad C., Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
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Spratt B.G., Parkhill J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                    Staphylococcus aureus subsp. aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=46170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                       SEQUENCE FROM N.A. STRAIN=ATCC 27664;
                                                                                                                                                                                                                                              Enterotoxin Q (Fragment).
                                                                                                                                                                                                                                                                                                                                                                        52
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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33.2%; Pred. No. 1.8e-17;
tive 39; Mismatches 76
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                                                                                                                                                                                                                                                                27,
27,
27,
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Last seq
Last ann
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                                                                                       enterotoxin
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                                                                                     genes
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Best Local S
Matches 63
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GO; GO:0009405; P:pathogenesis; IBA.
InterPro; IPR00892; Bact endotox.
InterPro; IPR006177; Bctr tox
InterPro; IPR006127; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strep tox.
InterPro; IPR008375; Staph_exotoxin.
InterPro; IPR008375; Staph_exotoxin.
InterPro; IPR008175; Staph_exotoxin.
InterPro; IPR006173; Staph_exotoxin.
              EMBL; U93688; AAC28968.1; -...
HSSP; P13380; IKTK.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strep_toxin.
InterPro; IPR006173; Stap/h tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox.C; 1.
PFAMT; PF00279; BACTRLTOXIN.
PROSITE; PR00279; BACTRLTOXIN.
PROSITE; PS00278; STAPH STREP TOXIN_2; 1
SEQUENCE 242 AA; 27720 MW; 28CB4F2EE
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Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PRINTS; PR01800; STAPHEXOTOXN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
NOW TEXT
                                                                                                                                                                                                                                                                                                                                         MEDLINE=98385824; PubMed=9720870; Lindsay J.A., Ruzin A., Ross H.F., Kurer "The gene for toxic shock toxin is carripathogenicity islands in Staphylococcus Mol. Microbiol. 29:527-543(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Staphylococcal enterotox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus. Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                   Barry P.C., Novick R
Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=RN4282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=entK;
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                                                                                                                                                                                                                                                                                      STRAIN=RN4282
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163 AA;
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ilarity 37.7%;
Conservative 27
                                                                                                                                                                                                                                    Novick R.P.;
TAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IrEMBLrel. 06,
IrEMBLrel. 06;
IrEMBLrel. 25,
l enterotoxin K
                    STAPH STREP_TOXIN_2; 1.
; 277\overline{2}0 MW; 28CB4F2EE68B66B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillales;
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Pred. No. 1.3e-17;
7; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4F7B02D47D600F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                          Kurepina N., Novick R.P.; carried by a family of mobile
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Staph_tox_OB.
InterPro; IPR006123; Staph_tox_OB.
InterPro; IPR006123; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02176; Stap_Strp_tox.C; 1.
Pfam; PF02876; Stap_Strp_tox.C; 1.
PRINTS; PR00279; STAPH_STREP_TOXIN 2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN 2; 1.
SEQUENCE 242 AA; 27727 MM; 207938B999DC.
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01-DEC-2001
01-OCT-2003
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Q93CC5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization and expression analysis of Staphylococcus aureus pathogenicity island 3. Implications for the evolution of staphylococcal pathogenicity islands.";
J. Biol. Chem. 277:13138-13147(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlievert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21935388; PubMed-11821418; DOI-10.1074/jbc.M111661200; Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               Similarity 72; Conser
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                                                                                                                                                                                                                                 LSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSTNKKLVTAQEIDVKLRKYLQEEYNIYGHNGTKKGEEYGHKSKFYSGFNIGKVTFHLNN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VQRGLIVFHSSE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKLDVFGISYNGQC-----NTKYIYGGVTA-TNEYLDKSRNIPINIWINGNHKTISTNK
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                                                VKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VQRGLIVFHSSE 190
                                                                                                                                      KKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDK 142
                                                                                                                                                                                      IDNLRNFYTKKDFVDLKDVKDNDTPIANQLQF----SNESY-DLISESKDFNKFSNFKG
    VSTNKKFVTAQEIDVKLRKYLQEEYNIYGHNGTKKGEEYGHKSKFYSGFNIGKVTFHLNN
                                                                                           KKLDVFGISYNGQC-----NTKYIYGGVTA-TNEYLDKSRNIPINIWINGNHKTISTNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales; Staphylococcus
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19,
25,
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                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                          Score 309; DB 2;
Pred. No. 2.2e-17;
0; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                          207938B999DC9A9A CRC64;
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                                                                                                                                                                                                                                                                                 26;
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       195
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ETXB_STAAU
ID ETXB
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X PubMed=15213324; DOI=10.1073/pnas.0402521101;

A Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

A Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

A Holden M.T.G., Feil E.J., Moore C.E., Hurst L., Atkin R., Barron A.,

A Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

A Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,

A Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,

A James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

A James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

A James K.D., Lennard N., Stevens K., Whitehead S., Barrell B.G.,

A Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

A Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

A Spratt B.G., Parkhill J.,

Tomplete genomes of two clinical Staphylococcus aureus strains:

Tevidence for the rapid evolution of virulence and drug resistance.";

Proc. Natl Acad. Sci. U.S.A. 101:9786-9791(2004).

R EMBL, BS571856; CAG409066.1; -

DR GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.
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Best Local
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InterPro; IPR006177; BctrI tox.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00779; BACTRITOXIN.
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Q6GFMB;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
P01552;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00278;
Complete proteome.
SEQUENCE 239 AA;
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Staphylococcus aureus (strain MRSA252).
Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                              GTSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDV
                                                                                                                                                                                                              GSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                            VSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTKSKFFSGFNTGKISFHLND
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X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).

WEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;

MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;

Papageorgiou A.C., Tranter H.S., Acharya K.R.;

Papageorgiou a.C., Tranter H.S., Acharya K.R.;

"Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors.";

J. MOl. Biol. 277:61-79(1998).

-I- FUNCTION: Staphylococcal enterotoxins cause the intoxication of annhylococcal food poisoning syndrome. The illness character of annhylococcal food poisoning syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.

MEDLINE=94203282; PubMed=8152483; DOI=10.1038/36871140;

MATCHINE=94203282; PubMed=8152483; DOI=10.1038/36871140;

MIDELINE=94203282; PubMed=8152483; DOI=10.1038/36871140;

Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;

"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huang I.-Y., Bergdoll M.S.;

"The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin and the complete amino acid sequence.";

J. Biol. Chem. 245:3518-3525(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., "Molecular cloning of staphylococcal enterotoxin B coli and Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Crystal structure of staphylococcal enterotoxin B, a superantigen,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones C.L., Khan S.A.; "Nucleotide sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=86168029;
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25-OCT-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B."; Immunity 9:807-816(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li H., Llera A., Tsuchiya D., Leder
Karjalainen K., Mariuzza R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
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                                                                                                                                                                               SUBCELLULAR LOCATION: SIMILARITY: Belongs to
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                                                                                                         entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation -
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InterPro; IPR00892; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006123; Staph/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006126; Staph tox OB.
Pfam; PF02876; Stap_Strp_tox C; 1.
Pfam; PF0123; Stap_Strp_toxin; 1.
Pfam; PF0123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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1D5X; X-ray; C=28-266.

1D5Z; X-ray; C=28-266.

1D6E; X-ray; C=28-266.

1SB3; X-ray; B/D=28-266.

1SB3; X-ray; @=28-266.

1SB3; X-ray; @=28-266.

1SB4; X-ray; @=28-266.

1SB4; X-ray; D/H=29-262.

1SBB; X-ray; D=28-265.

1SBB; X-ray; @=28-265.
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 DDN -> NND (in Ref. 3).
DQFLYFDLI -> NEFFDLIYL
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DIN -> NID (in Ref. 3).
QTD -> ENT (in Ref. 3).
NG -> GN (in Ref. 3).
Y -> YY (in Ref. 3).
D -> NG (in Ref. 3).
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SEQUENCE
                                                                                                              Pfam; PF01123; Stap_Strp_toxin; 1.

Pfam; PF02876; Stap_Strp_tox C; 1.

PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN 2; 1.

SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;
                                                                                                                                                                                                                                                                                    Staphylococcus aureus
Bacteria; Firmicutes;
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Similarity 33.6%;
82; Conservative 4:
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                                                            KSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITE-NKESDDQFLENTLLFKGFFTGH
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 TACMYGGVTLHDNNRLTEEKKV--PINLWI----DGKQTTVPIDKVKTSKKEVTVQELDLQ
                            PWYNDLLVDLGSK------K 103
                                                KPEQLN-----KASEF-TGLMDNMR--YLYDDKHVSEINIKAQEKFLQHDLLFK-----
                                                                                                                                                                                                                                                                                                                                                                                   YLTT 263
                                                                                                                                                                                                                                                                                                                                                                                                   YLYT 232
                 --INGSKID-
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                                                                              24.1%;
llarity 31.5%;
Conservative 49
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                                                                                                                                                                                                                                             PubMed=12807452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
31436 MW;
                GSKILKTEFNNNSLSDKYKNKNIDLFGTNYYYQCYFSADNMELNDGRLIE
                                                                                                                                                                                                                                                                                    Bacillales; Staphylococcus
                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                            Created)
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                                                                              Score 298; DB 2;
Pred. No. 1.9e-16;
9; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                            261
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                                                                                              Length 261;
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[1]
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          187
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                                                                                                                                        Conservative
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evidence for the rapid evolution of virulence and of proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
EMBL; BX571856; CAG40904.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR008123; Staph/Strept_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox OB.
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Pfam; PF02876; Stap_Strp_tox C; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
Complete proteome.
SEQUENCE 261 AA; 30547 MW; A407E960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.,
Complete genomes of two clinical Staphylococcus aureus strains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PubMed=15213324; DOI=10.1073/pnas.0402521101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain MRSA252).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                104 TACMYGGVTLHDNNRLTEEKKV--PINLWI---DGKQTTVPIDKVKTSKKEVTVQBLDLQ 158
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                                                       ARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDN 216
                                                                                                                                                                                                                                                    --INGSKID-GSKILKTEFNNNSLSDKYKNKNIDLFGTNYYYQCYFSADNMELNDGRLIE
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261 AA; 30547 MW; A407E960CC5974B0 CRC64;
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VRNYLLKHKNLYEFNS--SPYETGYIKFIEGNGHSFWYDMMPESGEKFYPTKYLLIYNDN
                                                                                                                        KTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVFENERNSLSFD-IPTNKKNITAQEIDYK
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31.5%; Pred. No. 1.9e-16;
tive 49; Mismatches 79
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Interpro; IPR008992; Bact endotox.
Interpro; IPR006177; BctrI tox.
Interpro; IPR006133; Stap/Strep_toxin.
Interpro; IPR006133; Stap/Strep_tox.
Interpro; IPR006133; Staph/Strept_tox.
Interpro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Stap_Strp_tox_C; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
Pfam; PF01123; Stap_Strp_toxIn; 1.
PRINTS; PR002779; BACTRLTOXIN.
PRINTS; PS002779; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Complete protecome; Signal; Toxin.
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P62561; P08095;
01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                           CHAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M10 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MGAS8232 / Serotype M18;
PubMed=11917108; DOI=10.1073/pnas.062526099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=speA; OrderedLocusNames=spyM18_0393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exotoxin type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever (By similarity).

SUBUNIT: Binds to major histocompatibility complex class II beta SIMILARITY: Belongs to the staphylococcal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Eleropean Bioinformatics Institute. There are no rest
  25
                                                 4
                                                                                                     118
                                                                                                                                 Similarity
SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VS
                                                 SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
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                                                                                                                                                                                                        128 B
29246 MW;
                                                                                                                              23.9%;
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Lactobacillales;
                                                                                                     45;
                                                                                                                                                                                                           Exotoxin type A.
By similarity.
54001FE4CCCBFCC3
                                                                                                                                 Pred.
                                                                                                                                                         Score 295.5;
                                                                                                                                                                                                                                                                                        By similarity.
                                                                                                        Mismatches
                                                                                                                                   No.
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                                                                                                     2.9e-16;
ches 92;
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MBL outstation -
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P62560; P08095;
01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                          the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).

MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;

Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,

Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,

O'Brien S.M., Tranter H.S., Acharya K.R.;

"Structural basis for the recognition of superantigen streptococcal

"Structural basis for the recognition of superantigen and T-cell

pyrogenic exotoxin A (SpeAl) by MHC class II molecules and T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEA
             EMBL; U40453; AAC48868.1; -.
EMBL; X03929; CAA27568.1; -.
PIR; A26152; A26152.
                                                                                                                                                                                                                                                                                                                                                          EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson L.P., L'Italien J.J., Schlievert P.M.; "Streptococcal pyrogenic exotoxin type A (scarlet related to Staphylococcus aureus enterotoxin B."; Mol. Gen. Genet. 203:354-356(1986).
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                     pyrogenic exotoxin A (SpeA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86284313; PubMed=3526093;
Johnson L.P., L'Italien J.J., Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weeks C.R., Ferretti
"Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=86166804; PubMed=3514452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=speA;
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                                                                                                                                                                                                                                                                                                                                                                         receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPE A).
                                                                                                                                                                                                                                                                                                        FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic
                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                             MISCELLANEOUS:
                                                                                                                                                                                                                                                                             SUBUNIT: Binds to major histocompatibility
                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                            J. 18:9-21(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin)
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                                                                                                                                                                                                                          Belongs
                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the type A streptococcal exotoxin gene from Streptococcus pyogenes bac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                toxin seems to be coded by baccarationing to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Scarlet
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Matches 81
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InterPro; IPR006177; Bctrl tox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PP02876; Stap Strp tox OB.
Pfam; PP01123; Stap Strp toxin; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
PROSITE; PS00277; STAPH STREP TOXIN 2; 1.
3D-structure; Signal; Toxin.
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PDB; 1FNV; X-ray; -.
PDB; 1FNW; X-ray; -.
PDB; 1HAS; X-ray; -.
PDB; 1LOX; X-ray; -.
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                                          SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VS
                                                              SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
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llarity 34.2%;
Conservative 4
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178
                                                                                   ; Score 295.5; DB 1;
; Pred. No. 2.9e-16;
45; Mismatches 92;
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VT -> MK (in Ref.
SQEVFAQQDPD ->
H -> Q (in Ref.
S -> N (in Ref.
NLQNIYFLYEGDP -
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I -> L (in Ref. 2).
TNKKMVTAQELDYK -> (
2).
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N (in Ref. 2).
N (in Ref. 2).
TEKIYIFFMRVTL
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(in Ref. 2)
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-> QIKNGNCSRISYT
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AC Q8K6K
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DT 01-0C
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Matches 61
Q6R1Y7;
Q6R1Y7;
05-JUL-2004
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05-JUL-2004
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A Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;

Rasigeev N., Volokhov D., Chizhikov V., Rasooly A.;

"Simultaneous analysis of multiple staphylococcal enterotoxin genes by

"I an oligonuclectide microarray assay.";

U. Clin. Microbiol. 42:2134-2143(2004).

REMBL; AV518772; AAR99712.1; -.

REMBL; AV518772; AAR99712.1; -.

REMBL; AV518772; AAR99712.1; -.

ROJ GO:0000575; Cleavtracellular; IEA.

GO; GO:000575; Cleavtracellular; IEA.

GO; GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

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ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Cleavtracellular; IEA.

ROJ GO:000575; Stap/Strap tox.

ROJ GO:000575; Stap/Strap tox.

ROJ GO:000575; Stap/Strap tox.

ROJ GO:000575; Stap/Strap TOXIN_2; 1.
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05-JUL-2004 (TREMBLrel. 27, Last sequence update)
05-JUL-2004 (TREMBLrel. 27, Last annotation updat
Enterotoxin type M variant (Fragment).
Staphylococcus aureus subsp. aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI TaxID-46170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15131181;
Sergeev N., Volokhov D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                      HSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHIDL
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                                                                                                                                                                                     PIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSD-----SFGGK-----VQRGLIVF 186
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HLNDGTSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDV
                                                                                                                                             STDKVSTNKKI VTAQEIDTKLRRYLQEEYNI YGFNDTNKGRNYGTKSKFFSGFNTGKI SF
                                                                                                                                                                                                                                                                                   KFKNRAVDVYGLSYSGYCL-----KNKYMYGGVTL-AGDYLEKSRCIPINLWVNGNHKTI
                                                                                                                                                                                                                                                                                                                       KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV
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177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%; Score 295; DB 2;
larity 37.7%; Pred. No. 2.1e-16;
Conservative 31; Mismatches 52
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EMBL; AP005142; BAC63655.1; --
PIR; A60108; A60108.

HSSP; P01552; 1SEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR00617; Bctr Itox.
InterPro; IPR00617; Bctr Itox.
InterPro; IPR006133; Stap/Strep toxin.
InterPro; IPR006133; Stap/Strep toxin.
InterPro; IPR006133; Staph tox OB.
Pfam; PF01133; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp toxin; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
 Q6XXM3;
Q6XXM3;
05-JUL-2004
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Genome Res. 13:1042-1055(2003).
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Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyas
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_tox.
InterPro; IPR006125; Staph_tox_OB.
InterPro; IPR006173; Staph_tox_OB.
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Letertre C., Perelle S., Dilasser F., Fach P.,
"Identification of a new putative enterotoxin SE
cluster of Staphylococcus aureus.";
J. Appl. Microbiol. 95:38-43(2003).
EMBL; AY205305; AAP41901.1; -.
GO: GO:000576; C:extracellular; IEA.
GO: GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008192; Bact endotox.
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Letertre C., Perelle S., Dilasser F., Fach P.;
"Identification of a new putative enterotoxin
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Pred. No. 6.6
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Matches 74
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Best Local
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HSSP; P13163; 1ESF.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Staph_toxin; 1.
Pfam; PF01123; Stap_strp_toxin; 1.
Pfam; PF02876; Stap_strp_toxin; 1.
PF0SITE; PS00278; STAPH_STREP_TOXIN_2; 1.
NON_TER; 207
SEQUENCE 207 AA; 23953 MM; AE71FC176E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7X0E8;
Q7X0E8;
01-OCT-2003
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InterPro; IPR006173; Staph.tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 261 AA; 30590 MW; D3D6CB0FBA124F58 CRC64;
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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01-OCT-2003 (TrEMBLrel. 25, La
01-MAR-2004 (TrEMBLrel. 26, La
Enterotoxin type I (Fragment).
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74; Conser
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KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK----
                                                                                                                         WYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE
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                                                                                                                                                                             NIKDL---SYAQGDIGVGNLRNFYTKYDYIDLKGVTDKNLPIANQLE-----FSTG--
                                                                                                                                                                                                                            NEKDLRKKSELORN-ALSNLRQIY----YYNEKAITENKESDDOFLENTLLFKGFFTGHP
                                                                             -TNDLISESNNWDEISKFKGKKMDIFGIDYNGPC----KTKYMYGGATL-SGQYLNSA
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                             23953 MW; AE71FC176E55842C CRC64;
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                                                                                                                                                                                                                                                                        Score 289.5; I
Pred. No. 7.3e-
33; Mismatches
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Best Local S
Matches 74
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R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR006123; Stap/Strep_toxin.

R InterPro; IPR006123; Stap/Strep_tox.

R InterPro; IPR006123; Staph/Strept_tox.

R InterPro; IPR006123; Staph/Strept_tox.

R InterPro; IPR006173; Staph tox OB.

R Pfam; PF01123; Stap Strp_toxin; 1.

R Pfam; PF02876; Stap Strp_toxin; 1.

R PROSITE; PS00277; STAPH STREP TOXIN 1; 1.

SEQUENCE 261 AA; 30563 MW; 2FBEDA126DA86C9A CRC64;
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Q6XXM4;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                Q7X0E7;
                                                                         Staphylococcus aureus. Bacteria; Firmicutes;
                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cluster of Staphylococcus aureus.";
J. Appl. Microbiol. 95:38-43(2003).
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SEQUENCE
                                                                                                                           Enterotoxin type I (Fragment).
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Letertre C., Perelle S., Dilasser F., Fach P.;
"Identification of a new putative enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=FRI137;
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                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.3%; Score 288.5; DB 2; 31.0%; Pred. No. 1.2e-15; tive 49; Mismatches 91;
                                                                               Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillales; Staphylococcus
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                                                                            Staphylococcus
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RESULT 68
Q7X0E9
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Best Local
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Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2003) to the EMBL/GenBan)
EMBL; AY291443; AAP78522.1; -.
HSSP; P13163; IESF.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008123; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006173; Stap/Strep_toxin.
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Q7X0E9;
01-OCT-2003
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HSSP; P13163; IESF.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006173; Staph_tox_OB.
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Pfam; PF02876; Stap_Strp_tox_C; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
NON_TER 218 218
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                           Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PROSITE; PS00278; STAPH_STREE_TOXIN_2; 1.
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01-OCT-2003 (TrEMBLrel. 25, Lan
01-MAR-2004 (TrEMBLrel. 26, Lan
Enterotoxin type I (Fragment).
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70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STDKIATNKKLYTAQEIDVKLRRYLQEEYNIYGHNNTGKGKEYGYKSKFYSGFNNGKVLF
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                                                                                                                                                  218 AA;
   Conservative
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                                      23.1%;
                                                                                                                                                  24994 MW; 698329CE49754350 CRC64;
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34.0%; Pred. No. 1.1e-15;
ive 34; Mismatches 69
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       34;
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   Score 286.5;
Pred. No. 1.4e
34; Mismatches
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Last annotation update)
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                                      5; DB 2;
1.4e-15;
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69;
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       33;
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23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN 78

RESULT

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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctrl_tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Staph_txrept_tox.
InterPro; IPR006123; Staph_txrept_tox.
InterPro; IPR006123; Staph_txrept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02176; Stap_Strp_tox_C; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
NON_TEP
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01-NOV-1996
01-NOV-1996
01-OCT-2003
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L13374; AAA26618.1; -.
HSSP; P23313; 1KLU.
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                                                                                                                             --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                      DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE
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                                RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                                                NLQNVLVRVY-ENKRNTISFE-VQTDKKSVTAQELDIKARNFLINKKNLYEFNS--SPYE
                                                                                                                                                                                                      ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNG
TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTT
                                                                                                                                                                                                                                                                                                         DLHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNISDKRLKNYDKVKT
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(TrEMBLrel.
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RESULT
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                                                                                                                      ETC3 STAAM STANDARD; PRT; 266 AA.

P233II;

01-NOV-1991 (Rel. 20, Created)

10-NOV-1991 (Rel. 20, Last sequence update)

125-OCT-2004 (Rel. 45, Last annotation update)

125-OCT-2004 (Rel. 45, Last annotation update)

13 Enterotoxin type C-3 precursor (SEC3).

14 Name=entC3; OrderedLocusNames=SAV2009, SA1817;

15 Staphylococcus aureus (strain Mu50 / ATCC 700699)

15 Staphylococcus aureus (strain N315), and

15 Staphylococcus aureus.

16 Staphylococcus aureus.

17 Staphylococcus aureus.

17 Staphylococcus aureus.

18 Staphylococcus aureus.

18 Staphylococcus aureus.

18 Staphylococcus aureus.

18 Staphylococcus aureus.
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Best Local
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MEDILINE=94011313; PubMed=8406814;

MEDILINE=94011313; PubMed=8406814;

Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";

Infect. Immun. 61:4254-4262(1993).

EMBL; L13375; AAA26619.1; -.

HSSP; P23313; IKLU.

HSSP; P23313; IKLU.
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Q06532;
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Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=1280;
  SEQUENCE FROM N.A. STRAIN=Mu50 / ATCC MEDLINE=21311952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stapp/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox OB.
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                                                                                                   NCBI_TaxID=158878,
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PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005576; C:extracellular; IEA.
GO:0009405; P:pathogenesis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGLIVFHSSEGSTVSYDLFDAQGQYPD---TLLRIYRDNKTINSENLHIDLYLYT
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ATCC 700699, and N315;
.952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA; 27642 MW; C77009F46BC8D645 CRC64;
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                                                                                                              1280;
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Last sequence tast annoted
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Pred. No. 1.8e-15,
9; Mismatches 9:
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TOXIN.
SIGNAL
CHAIN
DISULFID

Enterotoxin type C-3

HELIX
HELIX
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TURN
HELIX
STRAND
STRAND

27 266 137 37 44 48 48 65

PROSITE;

PS00277; STAPH_STREP_TOXIN_1; 1.
PS00278; STAPH_STREP_TOXIN_2; 1.
ture; Complete proteome; Enterotoxin;

Signal; Superantigen;

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EMBL; AP003364; BAB58171.1; -.

EMBL; AP003135; BAB43097.1; -.

EMBL; X51661; CAA35972.1; -.

PIR; S11885; S11885.

PDB; 1JCK; X-ray; B/D=28-266.

PDB; 1JWW; X-ray; D=28-266.

PDB; 1JWW; X-ray; D=28-266.

PDB; 1JWU; X-ray; D=28-266.

PDB; 1KLG; X-ray; D=28-266.

PDB; 1KLG; X-ray; D=28-266.

PDB; 1KLU; X-ray; D=28-266.

PDB; 1KLU; X-ray; D=28-266.

InterPro; IPR008992; Bact endotox.

InterPro; IPR006123; Stap/Strept toxin.

InterPro; IPR006123; Stap/Strept tox.

InterPro; IPR006123; Stap/Strept tox.

InterPro; IPR006124; Staph/strept tox.

InterPro; IPR006125; Staph/strept tox.

InterPro; IPR006126; Staph/strept tox.

InterPro; IPR006126; Staph/strept tox.

InterPro; IPR006126; Staph/strept tox.

IPRINTS; PR0279; Stap Strp tox. C; 1

PRINTS; PR0279; BACTRLTOXIN.

PRINTS; PR0279; BACTRLTOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR. MEDLLNE-97064178; PubMed-8906797; DOI=10.1038/384188a0; Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffacher C.V., Schlievert P.M., Karjalainen K., Mariuzza R.A.; "Crystal structure of a T-cell receptor beta-chain complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hovde C.J., Hackett S.P., Bohach G.A.;
"Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
sequence comparison of all three type C staphylococcal enterotoxins.";
Mol. Gen. Genet. 220:329-333(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characte by high fever, hypotension, diarrhea, shock, and in some cas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357:1225-1240(2001).
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Ito T.,
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inrect. Immun. 61:4254-426
EMBL; L13377; AAA26621.1;
PDB; 1CK1; X-ray; A=1-239
GO; GO:0005577
                                                                                                                                                                                                                                           Q06535;
Q06535;
Q1-NOV-1996
Q1-NOV-1996
                                               MEDLINE=94011313; PubMed=8406814;
Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
"Characterization of novel type C staphylococcal enterotoxins: biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
                                                                                                                                                                             Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales;
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01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Enterotoxin (Fragment).
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                                                                                                                                                            NCBI_TaxID=1280;
                                                                                                                                SEQUENCE FROM N.A.
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   C:extracellular;
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Last sequence
Last annotation
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Pred. No. 2.1e
49; Mismatches
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annotation update)
                                                                                                                                                                                Staphylococcus
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InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strept coxin.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PP0123; Stap Strp toxin; 1.
Pfam; PP02876; Stap Strp tox C; 1.
Pfam; PP02876; Stap Strp tox C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
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01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                   Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox C; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
NON_TEP_NON_TEP_TOXIN_2;
                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR008177; Bctr Lox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox_OB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type C enterotoxin (Fragment). Staphylococcus intermedius.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U91526; AAB50248.1;
HSSP; P23313; 1JWM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1285;
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Last annotation updat
  Score 283.5; 1
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44; Mismatches
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Best Local S
Matches 76
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EMBL; AP004824; BAB94624.1; -.

HSSP; B94071; ISTE.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005905; P:pathogenesis; IEA.

InterPro; IPR008192; Bact endotox.

InterPro; IPR006127; Bctr] tox.

InterPro; IPR006123; Staph/Strept toxin.

InterPro; IPR006123; Staph/Strept tox.

InterPro; IPR006123; Staph tox_OB.

InterPro; IPR006123; Staph tox_OB.

Pfam; PF01123; Stap Strp toxin; 1.

Pfam; PF01276; Stap Strp toxin; 1.

Pfam; PF02876; Stap Strp toxIN; 1.

PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.

Complete proteome.

SEQUENCE 266 AA; 30670 MM; 4C654659AA
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2003 (TrEMBLrel. 25,
ENTEROTOXIN TYPE C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=sec4; OrderedLocusNames=MW0759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBNXJ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8NXJ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto K., Hiramatsu K.; "Genome and virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=196620;
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                                                                                                                                                                     KLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGIT
                                                                                       LHDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY
                                                                                                                                                                                                                      GHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVT 112
                                                                                                                                                                                                                                                                                AESOPDPTPDELHKSSEF-TGTMGNMK--YLYDDHYVSATKVKSVDKFLAHDLIYNISDK 83
                                                                                                                                                                                                                                                                                                                                     SEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGNLONVLIRVY-ENKRNTISFD-VOTDKKSVTAQELDIKARNFLINKKNLYEFNS--SP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE--KKVPINIWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLHKSSEF-TGTMGNMKCLYDDYY----VSATKVKSVDKFLAHDLIYNISDKKLKNYDKV
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                                                       KHEGNHFDNGNLQNVLIRVY-ENKRNTISFE-VQTDKKSVTAQELDIKARNFLINKKNLY
  NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30670 MW; 4C654659AA48120F
                                                                                                                                                                                                                                                                                                                                                                                         22.9%; Score 283.5; DB 2 31.1%; Pred. No. 3.1e-15; tive 50; Mismatches 99
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Bacillales; Staphylococcus
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RESULT 76
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ID ETC2
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Q06533;
Q106533;
Q100V-1996 (TrEMBLrel. 01, Le
C10V-1996 (TrEMBLrel. 25, L
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Best Local Similarity
Matches 76; Conser
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EMBL; L13778; AAA26622.1; -.

HSSP; P34071; ISTE.

GO; GO:000576; C:extracellular; IEA.
GO; GO:0005976; C:extracellular; IEA.
InterPro; IPR00617; Bact_endotox.
InterPro; IPR00617; Bact_lox.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006123; Staph tox_OB.

Pfam; PF0123; Stap_Strp_tox.C; 1.
Pfam; PF02876; Staph_Strp_tox.C; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN_1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.

PRON_TER; PS00278; STAPH_STREP_TOXIN_2; 1.
STAAU
ETC2 STAAU
P34071;
01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94011313; PubMed=8406814;
Marr J.C., Lyon J.D., Roberson J.R., Lupher M., E
"Characterization of novel type C staphylococcal
biological and evolutionary implications.";
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
                                                                                                                                                                                                                                                         LYI
                                                                                                                                                                                                                                                                                                                                                         SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLY 229
                                                                                                                                                                                                                                                                                                             FNS--SPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKRVKIEVH
                                                                                                                                                                                                                                                                                                                                                                                                                         HEGNHFDNGNLQNVLIRVY-ENKRNTISFE-VQTDKKSVTAQELDIKARNFLINKKNLYE
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     (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                  236
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                                                          STANDARD;
     28,
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  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 282.5; D
; Pred. No. 3.3e-
49; Mismatches
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InterPro; IPRO08992; Bact endotox.
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InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap Strp toxin; 1.
PFAm; PF01123; Stap Strp toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN 1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN 2; 1.
3D-structure; Direct protein sequencing; Enginal; Superantigen; Toxin; Zinc.
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MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;

"A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity.";

J. Mol. Biol. 269:270-280(1997).
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MEDLINE=96027099; PubMed=7582894; DOI=10.1016/S0969-2126(01)00212-X;
Papageorgiou A.C.. Acharya K.R., Shapiro R., Passalacqua E.F.,
Brehm R.D., Tranter H.S.;
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Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Residues defining V beta specificity in staphylococcal
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Bacteria; Firmicutes;
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                                                                                 Signal; Superantigen; SIGNAL 1 2
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; 114P; X-ray; A=28-266.
; 114Q; X-ray; A=28-266.
; 114R; X-ray; A=28-266.
; 114X; X-ray; A=28-266.
; 15E2; X-ray; @=28-266.
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for the toxin interaction with
SUBCELLULAR LOCATION: Secreted
SIMILARITY: Belongs to the stay
family:
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FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness character by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and in some case by high fever, hypotension, diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, shock, and diarrhea, s
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strept toxin.
InterPro; IPR006123; Staph/Strept tox.
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EMBL; AY291446; AAP78528.1; -
HSSP; H3163; ISSF,
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006193; Bact endotox.
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InterPro; IPR006173; Stap/Strep tox OB.
Pfam; PF01276; Stap/Strp tox C; 1.
PFGM; PF02876; Stap/Strp tox C; 1.
PROSITE; PS00278; STAPH_STREF_TOXIN_2; 1.
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05-JUL-2004
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"A strategy based on 5' nuclease multiplex PCR to detect enterotoxin genes sea to sej of Staphylococcus aureus.";
Mol. Cell. Probes 17:227-235(2003).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Enterotoxin seb variant (Fragment).
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67; Conserv
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STAPH_STREP_TOXIN_1;
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Best Local S
Matches 78
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                           Query Match
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InterPro; IPR006127; Bctrl tox.
InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006126; Staph tox OB.
InterPro; IPR006173; Staph tox OB.
Pfam; PF02123; Stap Strp toxin; 1.
Pfam; PF02176; Stap Strp toxin; 1.
PROSITE; PR00279; BACTRLTOXIN
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY450554; AAR20496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu M., Zhang C.;
Submitted (OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                        Local
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 DLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD
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                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                   HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTL 113
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                                                                         LKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITK 117
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                                                                                                                                                                    ESOPDPTPDELHKSSEF-TGTMGNMK--YLYDDHYVSATKVMSVDKFLAHDLIYNISDKK
                                                                                                                                                                                                              EKSEEINEKDLRKKSELORNALSNLROIYYYNEKAITENK-ESDDOFLENTLLFKGFFTG
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27585 MW;
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                                                                                                                                                                                                                                                                  49; Mismatches
                                                                                                                                                                                                                                                          Score 280.5; DB 2;
Pred. No. 4.8e-15;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                            enterotoxin C2.
; 6A7828027F893822 CRC64;
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J. Exp. Med. 174:1271-1274(1991).

EMBL; X61573; CAA43771.1; -.

PIR; $18789; $218789.

HSSP; P01552; 1SEB.

GO; GO:0005576.
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SEQUENCE
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Pfam; PF02876; Stap_Strp_tox C; 1.
PRINTS; PR00279; BAGTELTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006137; Stap/Strept toxin.
InterPro; IPR006133; Staph/Strept toxin.
InterPro; IPR006173; Staph/Strept toxin.
InterPro; IPR006173; Staph/Strept tox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92044323; PubMed=1940804; Nelson K., Schlievert P.M., Selander R.K.,
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                            180
                                                                            134
                                                                                                                                                                             74
                                                                                                                                                                                                                      61 HPWYNDLLVDLGSKDATNKYKGKKYDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL
                                                                                                                                                                                                                                                                                                   4 SEEINEKDLRKKSELQRNAL-SNLRQIY--YYNEKAITENKESDDQFLENTLLFKGFFTG
                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                           GLNYDKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCRNAKRRACIYGGVINHEGNHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEGNHFDNGNLQNVLIRVY-ENKRNTISFE-VQTDKKSVTAQELDIKARNFLINKKNLYE
QRGLIVFHSSEGSTVSYDLFDAQGQYPDTLLRIYRDNKTINSENLHI
                                                                          EIPKNILVKVSIDGIQ-
                                                                                                                        TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV
                                                                                                                                                                                                                                                                         SQEVFAQQDPNPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSVDQLLSHDLIYN---VS
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236
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27575 MW;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 279.5; DB Pred. No. 5.7e-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
type A exotoxin.
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01-MAR-2001
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                              268
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact = ndotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox_OB.
InterPro; IPR006173; Staph tox_OB.
Pfam; PF01123; Staph Strp_toxin; 1.
R Pfam; PF02876; Stap_Strp_toxin; 1.
R PFNNTS; PR00279; BACTRITOXIN.
R PRNSTTE; PS00279; BACTRITOXIN.
R PROSITE; PS00279; STAPH STREP_TOXIN_1; 1.
R PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;
P97163; P97164;
01-MAY-1997 (TTEMBLrel. 03, Created)
01-MAY-1997 (TTEMBLrel. 03, Last sequence update)
05-JUL-2004 (TTEMBLrel. 27, Last annotation update)
Type A exotoxin precursor (Fragment).
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of a putative pathogenicity island from Staphylococcus aureus encoding multiple superantigens."; J. Bacteriol. 183:63-70(2001).
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Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 NSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 KLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ABSOPDPTPDELHKASKF-TGLMENMKVL--YDDRYVSATKVKSVDKFLAHDLIYNISDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHDNNRLTBEK--KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVT
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HSSP; P01552; 1SEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR008192; Bact endotox.
InterPro; IPR008177; BctrI tox.
InterPro; IPR008123; Stap/Strep_toxin.
InterPro; IPR008126; Staph/Strept tox.
InterPro; IPR008126; Staph/Strept tox.
InterPro; IPR008173; Staph_tox.OB.
Pfam; PF01123; Stap_strp_tox.II; 1.
Pfam; PF02876; Stap_strp_tox.II; 1.
PROSITE; PR00277; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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J. Exp. Med. 174:1271-1274(1991).
EMBL; X61556; CAA43754.1; -.
EMBL; X61555; CAA43753.1; -.
EMBL; X61558; CAA43755.1; -.
EMBL; X61558; CAA43756.1; -.
EMBL; X61559; CAA43757.1; -.
EMBL; X61559; CAA43757.1; -.
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Staphylococcus aureus.
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43; Mismatches
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence upon 01-DCT-2003 (TrEMBLrel. 25, Last annotation upon progenic exotoxin A (Fragment).
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR00892; Bact endotox.
InterPro; IPR008177; Bctrl cox.
InterPro; IPR008123; Stap/Strep toxin.
InterPro; IPR008123; Staph/Strept tox.
InterPro; IPR008123; Staph tox OB.
Pfam; PF01123; Staph Strp toxin; 1.
Pfam; PF02173; Staph Strp toxin; 1.
Pfam; PF02876; Staph Strp toxin; 1.
Pfam; PF02876; Staph Strp ToxIn; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
NON TER
            MEDLINE=94011313; PubMed=8406814;
Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22508029; PubMed=12620634;
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               Q985Z4, PRELIMINARY;
Q985Z4, 17EMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRUTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
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InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph_tox_OB.
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  121F8460992818F8 CRC64;
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GO; GO:000576; C:extracellular; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008192; Bact endotox.
InterPro; IPR006177; BctrI tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR00613; Staph tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02176; Stap_Strp_toxin; 1.
Pfam; PF00277; STAPH_STREP_TOXIN_1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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01-MAY-2000
01-MAY-2000
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Van den Bussche R.A., I
Mol. Phylogenet. Evol.
HSSP; P34071; 114X.
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                                                                                                                                                                                                                    70 DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEB
                                                                                                                                                                                                                                                                                                                          11 DIRKKSELQRNALSNIRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
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RGLIVFHSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSENLHIDLYLYT 232
                                                                        --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
                                                                                                                                                                                                                                                                           DLHKSSEF-TGTMGNMK--YLYDDNYVSATKVKSVDKFLAHDLIYNISDKRLKNYDKVKT
                                                                                                                                                                        ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNG
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234 AA;
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.A., Lyon J.D., Bohach G.A.;
Evol. 2:281-292(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                  22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27122 MW; D6A7B45FB9810052 CRC64;
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Last annotation update)
(Fragment).
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Pred. No. 8.2e-15;
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nes 95;
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph tox OB.
InterPro; IPR006127; Staph tox OB.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp toxin; 1.
PROSITE; PR00277; STAPH_STREP_TOXIN_1; 1.
                                                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene encoding pyrogenic exotoxin A (scarlet fever toxin)
Streptococcus pyogenes.";
J. Exp. Med. 174:1271-1274(1991).
EMBL; X61569; CAA43766.1; -.
EMBL; X61570; CAA43766.1; -.
EMBL; X61570; CAA43769.1; -.
EMBL; X61572; CAA43770.1; -.
EMBL; X61572; CAA43770.1; -.
PIR; A60108; A60108.
                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MGAS485, MGAS158, MGAS491, MGAS495, an MEDLINE=92044323; PubMed=1940804; Nelson K., Schlievert P.M., Selander R.K., Mu "Characterization and clonal distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q54779 PRELIMINARY; PRT; 236 AA.
Q54779, Q54736; Q54740; Q54741;
Q1-NOV-1996 (TERMBLrel. 01, Created)
Q1-NOV-1996 (TERMBLrel. 01, Last sequence update)
Q5-JUL-2004 (TERMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type A exotoxin precursor (Fragment).
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PROSITE; PS00278; STAPH_STREP_TOXIN_2;
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                                                                                                                                                                     61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC-AGGTPNKTACMYGGVTLHDNNRL
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                                                                                                                                                                                                                                                            . Similarity 77; Conserv
                                                                                             GPNYDKLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHL
                                                                                                                                                                                                                       SEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG
                                                                  QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINSENLHI 226
                                                                                                                                                                                                        SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VS
                                         ETGYTKFIPKNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDSNTSQI
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llarity 33.3%;
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                                                                                                                                                                                                                                                         Score 277.5; DB 2; Length 236; Pred. No. 8.3e-15; Indels 19;
                                                                                                                                                                                                                                                                                                                                              type A
                                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                                                                                              exotoxin
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Q57453
ID Q5745
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AC Q5745
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DE Type
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Matches 77
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Bessen D.E., Izzo M.W., Fiorentino T.R., Ca
Hollingshead S.K., Beall B.;
"Genetic linkage of exotoxin alleles and em
tropism in group A streptococci.";
J. Infect. Dis. 179:627-636 (1999).
EMBL; AF055698; AAD11624.1; -.
PIR; A60108; A60108
HSSP; P01552; 1SEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008992; Bact endotox.
InterPro; IPR006127; Bctr¹ tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph_tox_OB.
InterPro; IPR006173; Staph_tox_OB.
InterPro; IPR006173; Staph_tox_OB.
InterPro; IPR006173; Staph_tox_OB.
IPFam; PF01123; Stap Strp_tox(C; 1.
Pfam; PF02876; Stap Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1: 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
NON_TER
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Q9R931;
01-MAY-2000
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NON TER
SEQUENCE
                                                                Q57453 PRELIMINARY; PRT; 236 AA. Q57453; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
           Streptococcus pyogenes. Bacteria; Firmicutes; I
                                      Type A exotoxin precursor (Fragment) Name=speA;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                                                                                                        TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
                                                                                                                                                                                       ETGYIKFIPKNKESFWFDFFPEPEFTQSKY----LMIYKDNETLDS
                                                                                                                                                                                                                  QRGLIVFHSSEGSTVSYDLFD----AQGQYPDTLLRIYRDNKTINS 221
                                                                                                                                                                                                                                               EIPKKIVVKVSIDGIQ-SLSFD-IETNKKMVTAQELDYKVRKYLTDNKQLYTNGP--SKY
                                                                                                                                                                                                                                                                                                                                                            SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYN---VS
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222 AA;
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25759 MW; 48BB7ADDCD91FBA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                22.3%; Score 276.5; DB 2; 34.1%; Pred. No. 9.3e-15; tive 43; Mismatches 87;
              Lactobacillales;
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Last sequence up
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              Streptococcaceae;
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; BctrI_tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph_tox_OB.
InterPro; IPR0061273; Staph_tox_OB.
InterPro; IPR0061373; Staph_tox_OB.
Pfam; PF01123; Stap_strp_toxin; 1.
Pfam; PF02876; Stap_strp_tox C; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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J. EXD. Med. 174:1271-1274(1991).
EMBL; X61562; CAA43760.1; -.
EMBL; X61561; CAA43759.1; -.
EMBL; X61563; CAA43761.1; -.
EMBL; X61565; CAA43763.1; -.
EMBL; X61566; CAA43763.1; -.
EMBL; X61566; CAA43763.1; -.
EMBL; X61566; CAA43763.1; -.
EMBL; X61567; CAA43765.1; -.
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EMBL; X61567; CAA43765.1; -.
EMBL; X61567; CAA43765.1; -.
EMBL; X61
                                                                                                                            Q06534;
Q06534;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2003
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STRAIN=MGAS156, MGAS250, MGAS256,
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[1]
                                                            Staphylococcus aureus. Bacteria; Firmicutes;
  SEQUENCE FROM N.A.
                                    NCBI_TaxID=1280;
                                                                                                          Enterotoxin (Fragment).
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                                                               Bacillales; Staphylococcus
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                                                                                                                            Created)
Last sequence update)
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR00817; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006123; Staph/Strept tox.
InterPro; IPR006123; Staph tox_OB.
InterPro; IPR006123; Staph tox_OB.
InterPro; IPR00613; Staph tox_OB.
InterPro; IPR00613; Staph tox_C; 1.
Pfam; PP01123; Stap_Strp_tox_C; 1.
Pfam; PP02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
NON_TER
SEQUENCE 239 AA; 27517 MW; F354742619
                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Weller;
MEDLINE=94222556; PubM
Reda K.B., Kapur V., M
Rich R.R.;
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Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L13379; AAA26
HSSP; P34071; 114X.
"Molecular characterization and phylogenetic distribution streptococcal superantigen gene (ssa) from Streptococcus Infect. Immun. 62:1867-1874(1994).

EMBL; L29565; AAA65928.1; -.

DBB; L3XT; X-ray; A/B=27-256.

GO; GO:000576; C:axtracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                              PubMed=8168951;
V., Mollick J.A., Lamphear J.G.,
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InterPro; IPR006177; BcttI_tox.
InterPro; IPR006173; Stap/Strept_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox OB.
Pfam; pF001123; Stap_Strp_toxin; 1.
Pfam; pF001273; Stap_Strp_toxin; 1.
Pfam; pF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 260 AA; 29797 MW; 2DD96017DE9D4F49 CRO
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                              MEDLINE=96178602; PubMed=8606073;
Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R R.
"Phylogenetic distribution of streptococcal superantigen SSA allelic
variants provides evidence for horizontal transfer of ssa within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94222556; PubMed=8168951; Reda K.B., Kapur V., Mollick J.A. Rich R.R.;
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Pred. No. 4.3e-14;
7; Mismatches 98
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InterPro; IPRO06177; Bctr Tox.

InterPro; IPRO06177; Bctr Tox.

InterPro; IPRO06178; Stap/Strept toxin.

InterPro; IPRO06178; Staph tox OB.

InterPro; IPRO06178; Staph tox OB.

Pfam; PF01123; Stap Strp toxin; 1.

Pfam; PF01123; Stap Strp toxin; 1.

PRINTS; PR00279; BACTRITOXIN.

PROSITE; PS00277; STAPH_STREP TOXIN 1; 1.

PROSITE; PS00277; STAPH_STREP TOXIN 2; 1.

PROSITE; PS00277; STAPH_STREP TOXIN 2; 1.

SEQUENCE 260 AA; 29767 MW; EAIPB7CCAE80F99B CR
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Q79X14;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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Pfam; PF02876; Stap_Strp_tox C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN 2; 1.
SEQUENCE 260 AA; 29836 MW; C122141693B42AD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005144; BAC64214.1; GO; GO:0005576; C:extracellular; IEAGO; GO:0009405; P:pathogenesis; IEA
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Genome Res. 13:1042-1055(2003).
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Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales;
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Best Local S
Matches 78
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GG; GG:0005405; P:pathogenesis; IEA.
InterPro; IPR008192; Bact_lox.
InterPro; IPR008173; Bact_lox.
InterPro; IPR008123; Stap/Strep_toxin.
InterPro; IPR008123; Stap/Strept tox.
InterPro; IPR008173; Staphtox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxIN.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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Q54739; Q54737;
01-NOV-1996 (TREMBLEGI. C
01-NOV-1996 (TREMBLEGI. C
25-OCT-2004 (TREMBLEGI. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular characterization and phylogenetic distribution of the streptococcal superantigen gene (ssa) from Streptococcus pyogener Infect. Immun. 62:1867-1874(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MGAS
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EMBL; U48792; AABO2148.1; -.
HSSP; Q54971; 1BXT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94222556; PubMed=8168951; Reda K.B., Kapur V., Mollick J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R R., Phylogenetic distribution of streptococcal superantigen SSA allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.B., Kapur V.,
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NDLLVDLGSKDATNKYKGKKVDLYGAYYGYQCAGGTPN----KTACMYGGVTLHDNNRL 119
                                                                                                                               EEINEKDLRKKSELORNALSNLROIYYYNEKAITENKESDDOFLENTLLFKGFFTGHPWY
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                                                                                                                                                                                     Conservative
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                                                                                 KSSQFTGVMGNLRCL-YDNHFVEGTNVRSTGQLLQHDLIFPIKDLKLKNY
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Last sequence update)
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InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006123; Staph/Strept_tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF02876; Stap_Strp_toxin; 1.
Pfam; PF01123; Stap_Strp_toxin; 1.
PF1NTS; PR00279; BACTELTOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
Direct protein sequencing; Enterotoxin; Signate Toxin = 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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SEQUENCE FROM N.A.
MEDLINE-88038352; PubMed=2823067;
Bohach G.A., Schlievert P.M.;
Bohach G.A., Schlievert P.M.;
"Nucleotide sequence of the staphylococcal enterotoxin "Nucleotide sequence of the staphylococcal enterotoxin relatedness to other pyrogenic toxins.";
Gen. Genet. 209:15-20(1987).
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P01553;
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DISULFID
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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01-UAN-1990 (Rel. 13, Last sequence update)
05-UII-2004 (Rel. 44, Last annotation update)
Enterotoxin type C-1 precursor (SEC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete amino acid sequence of staphylococcal enterotoxin C1.";
J. Biol. Chem. 258:6300-6306 (1983).
-:- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus. Bacteria; Firmicutes;
                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X05815; CAA29260.1; -. PIR; S06356; ENSAC1. HSSP; P34071; 114X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt J.J., Spero L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008992;
InterPro; IPR006177;
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SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
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A Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,

A Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,

James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

A James K.D., Lennard N., Line A., Mayes R., Moule S., Sanders M.,

Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.;

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InterPro; IPR006177; Bctr1 tox.
InterPro; IPR006173; Stap/Strep toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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Q6GFN2; PRELIMINARY;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Bacteria; Firmicutes; Bacillales; Staph
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                    SQPDPKIDE---LNKVSDYKSNKGTMGNVMNLYMSPPVEGRGVINSR----QFLSHDLIFP
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1; Mismatches 101;
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Best Local Similarity
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InterPro; IPR008177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap Strp_toxin; 1.
Pfam; PF012876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZNF2;
Q9ZNF2;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB016487; BAA36693.1; -.
HSSP; P01552; ISEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abe J., Ito Y., Onimaru M., Kohsaka T., "Characterization and distribution of a superantigen produced by Staphylococcus Microbiol. Immunol. 44:79-88(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterotoxin type Gv.
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20260630; PubMed=10803494;
                                                                                                                                           172
254
                                           229
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                                                                                                                                                                                              141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                          66 DLLVDLGSKDATNKYKGKKVDLYGAYYGYQCA-------GGTPNKTACMYGGVTL 113
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FLNT
                                           YLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00278; STAPH_STREP_TOXIN_2; 1.
258 AA; 29839 MW; 1229246D83F4FB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACMYGGVTLH---DNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARH
                                                                                                                                           SDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDT---LLRIYRDNKTINSENLHIDL
                                                                                                                                                                                              NSSENER----DKLITVQVTIDNRQSLG--FTITTNKNMVTIQELDYKARHWLTKEKKLYE
                                                                                                                                                                                                                                                                                                EVKTELENTELANNYKGKKVDIFGVPYFYTCIIPKSEPDINQNFGG-----CCMYGGLTF 140
                                                                                                                                                                                                                                                                                                                                                                                             ELNKVSDYKSNKGTMGNVMNLYMSPPVEGRGVINSR----QFLSHDLIFP---IEYKSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                         DLRKKSELORN--ALSNLRQIYY---YNEKAITENKESDDOFLENTLLFKGFFTGHPWYN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDSKSIKMEVFLNT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSENTHIDTATAL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLTKEKKLYEFD--GSAFESGYIKFTEKNNTSFWFDLFPKKELVPFVPYKFLNIYGDNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGQYPDT---LLRIYRDNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CCMYGGLTFNSSENER---DKLITVQVTIDNRQSLG--FTITTNKNMVTIQELDYKARH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IEYKSYNEVKTELENTELANNYKGKKVDIFGVPYFYTCIIPKSEPDINQNFGG---- 131
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                                                                                            FD--GSAFESGYIKFTEKNNTSFWFDLFPKKELVPFVPYKFLNIYGDNKVVDSKSIKMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 10, (TrEMBLrel. 10, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                              232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 262.5; DB 2; 29.5%; Pred. No. 1.6e-13; tive 49; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takeda T.;
new enterotoxin-related
aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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228

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RESULT 98
Q6XZE7
RESULT 99
Q764P
ID Q764P
AC Q764P
AC Q764P
DT 05-JU
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Best Local
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                   Q764P6;
Q764P6;
05-JUL-2004;
05-JUL-2004;
05-JUL-2004;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Enterotoxin sec variant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6XZE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1280;
                             Staphylococcus intermedius.
Bacteria; Firmicutes; Bacillales;
                                                 Name=se-int;
SEQUENCE FROM N.A.
                 NCBI_TaxID=1285;
                                                          Enterotoxin precursor.
                                                                                                                                                             176
                                                                                                                                                                                                    120
                                                                                                                                                                                                                   123 K--KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ
                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                        11 DLRKKSELQRNALSNLRQIYYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV
                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                               PS00277; STAPH_STREP_TOXIN_1;
PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                               DLGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTEE
                                                                                                                                                                             RGLIVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENL
                                                                                                                                                                                                                                             ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNG
                                                                                                                                                                                                                                                                                    ELHKASKF-TGLMENMKVL--YDDRYVSATKVKSVDKFLAHDLIYNISDKKLKNYDKVKT
                                                                                                                                                            TGYIKFIENNGNTFWYDMMPAPGDKFEQSKYLMMYNDNKTVDSKSV 221
                                                                                                                                                                                                   KLQNVLIRVY-ENKRNTISFE-VQTDKKSVTAQELDIKARNFLINKKNIYEFNS--SPYE
                                                                                                                                                                                                                                                                                                                                                                   222 AA;
                                                                   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          222
; 25784 MW;
                                                                                                                                                                                                                                                                                                                           21.0%; Score 259.5; DB 2
31.0%; Pred. No. 2.3e-13;
tive 48; Mismatches 89
                                                                    27,
27,
27,
                                                                    Last
Last
                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                     67A0546FF3CD73B1 CRC64;
                                                                    sequence update) annotation updat
                              Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
                                                                                                             264
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                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                    update)
                                                                                                                                                                                                                                                                                                                             89; Indels
                                                                                                                                                                                                                                                                                                                                              Length 222;
                                                                                                                                                                                                                                                                                                                             19;
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RESULT 100
Q9RQQ5
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Best Local
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InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PP01123; Stap Strp_toxin; 1.
Pfam; PP02876; Stap Strp_tox C; 1.
Pfam; PP02876; Stap Strp_tox C; 1.
PRINTS; PR00279; BACTRITOXIN.
Streptococcus pyogenes.";

J. Exp. Med. 189:89-102(1999).

EMBL; AF086626; AAD52087.1; -

PDB; 1ETG; X-ray; A/B=1-209.

PDB; 1EU3; X-ray; A/B=1-209.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008992; Bact endotox.

InterPro; IPR008177; BctrI_tox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
SIGNAL
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"Identification and prevalence of an enterotoxin-related gene, in Staphylcoccus intermedius isolates from dogs and pigeons.";

J. Appl. Microbiol. 96:1361-1366 (2004).

EMBL; AB116378; BAD13763.1; --

EMBL; AB116378; BAD13763.1; --

EO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mitogenic exotoxin Z 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Futagawa-Saito K., Suzuki M., Ohsawa M., Ohshima S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RQQ5;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                    MEDLINE=99093428; PubMed=9874566;
Proft T., Moffatt S.L., Berkahn C.J.,
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=2035;
                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes
Bacteria; Firmicutes; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=smez-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RQQ5
                                                                                                                                                                                                                          "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 LGSKDATNKYKGKKVDLYGAYYGYQC-----AGGTPNKTACMYGGVTLHDNNRLTBEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRKKSELQRNALSNLRQIYYYNEKAITE-NKESDDQFLENTLLFKGFFTGHPWYNDLLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00277; STAPH_STREP_TOXIN_1; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASKELAQKYRNKQVDIFGANYYVNCYFSGKEKGNEEDNGKTCMYGGVTNYBGNHLDNHK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVFHSSEGSTVSYDLFDAQGQ--YPDTLLRIYRDNKTINSENLHIDLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQTİYVKVFENSKHIITFEIQADKKLVTAQELDAKARKFLIDKLNLY--EFKGSPYETGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKFIENDDKSFWYDLMPPPGNNFNQSKYLTMYSDNKTVESEDIKIEVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
28
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264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 256.5;
Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
; 52330A55E4CE0E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 med. No. 5.1e-13;
Mismatches 104;
                                                                                                                                                                                                                               얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                       Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                    J.D.;
                                                                                                                                                                                                                          superantigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
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Search completed: July 26, 2005, 11:08:24 Job time: 182 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.7%; Score 256; DB 2; Length 209; Best Local Similarity 27.4%; Pred. No. 4.2e-13; Matches 66; Conservative 51; Mismatches 58; Indels 66; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF021876; Stap_Strp_tox C; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PR00279; STAPH_STREP_TOXIN_2; 1.
NOW TER 1 1 mitogenic exotoxin Z 2.
CHAIN <1 209
SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;
                                                                                                                                          148 YSS---GSSYKSGRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLD 204
                                                                                                                                                                                                          205 I 205
                                                                                                      228 L 228
                                                                                                                                                          170 YNSDSFGGKVQRGLIVFHSSEGS-TVSYDLFDAQGQYPDTLLRIYRDNKTINSENL-HID 227
                                                                                                                                                                                                                                                                               33 LVTKKLDVRDARDFFINSEMDEYAANDFKTGDKIAVFSVPFDWNYLSKG---KVTAYTYG
                                                                                                                                                                                                                                                                                                                71 ----LGSKDATNKYKGKKVDLYGAY------YGYQCAGGTPNKTACMYG 109
                                                                                                                                                                                                                                                                                                                                                                                     17 ELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD----- 70
                                                                                                                                                                                                                                                                                                                                                      2 EVDNNSL--LRNIY------STIVYE-----YSDIVIDFKTSHN 32
                                                                                                                                                                                                                                                                                 89
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